

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gallatin, W. Michael
Kilgannon, Patrick D.
- (ii) TITLE OF INVENTION: ICAM-4 Materials and Methods
- (iii) NUMBER OF SEQUENCES: 42
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
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 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: United States of America
 - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/827,689
 - (B) FILING DATE: 27-JAN-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/889,724
 - (B) FILING DATE: 26-MAY-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/894,061
 - (B) FILING DATE: 05-JUN-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/009,266
 - (B) FILING DATE: 22-JAN-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/102,852
 - (B) FILING DATE: 05-AUG-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/245,295
 - (B) FILING DATE: 18-MAY-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/485,604
 - (B) FILING DATE: 07-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: WILLIAMS, JR. JOSEPH A.
 - (B) REGISTRATION NUMBER: 38,659
 - (C) REFERENCE/DOCKET NUMBER: 27866/33321

(ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2988 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 61..2814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATTCGATCA	CTCGCGCTCC	CCTCGCCTTC	TGCGCTCTCC	CCTCCCTGCG	AGCGGCGGCA	60
ATG CCG GGG CCT TCA CCA GGG CTG CGC CGA ACG CTC CTC GGC CTC TGG	108					
Met Pro Gly Pro Ser Pro Gly Leu Arg Arg Thr Leu Leu Gly Leu Trp						
1 5 10 15						
GCT GCC CTG GGC CTG GGG ATC CTA GGC ATC TCA GCG GTC GCG CTA GAA	156					
Ala Ala Leu Gly Leu Gly Ile Leu Gly Ile Ser Ala Val Ala Leu Glu						
20 25 30						
CCT TTC TGG GCG GAC CTT CAG CCC CGC GTG GCG CTC GTG GAG CGC GGG	204					
Pro Phe Trp Ala Asp Leu Gln Pro Arg Val Ala Leu Val Glu Arg Gly						
35 40 45						
GGC TCG CTG TGG CTC AAC TGC AGC ACT AAC TGT CCG AGG CCG GAG CGC	252					
Gly Ser Leu Trp Leu Asn Cys Ser Thr Asn Cys Pro Arg Pro Glu Arg						
50 55 60						
GGT GGC CTG GAG ACC TCG CTA CGC CGA AAC GGG ACC CAG AGG GGT CTG	300					
Gly Gly Leu Glu Thr Ser Leu Arg Arg Asn Gly Thr Gln Arg Gly Leu						
65 70 75 80						
CGC TGG CTG GCT CGA CAG CTG GTG GAC ATC CGA GAG CCT GAA ACC CAG	348					
Arg Trp Leu Ala Arg Gln Leu Val Asp Ile Arg Glu Pro Glu Thr Gln						
85 90 95						
CCG GTC TGC TTC TTC CGC TGC GCG CGC CGC ACA CTC CAA GCG CGT GGG	396					
Pro Val Cys Phe Phe Arg Cys Ala Arg Arg Thr Leu Gln Ala Arg Gly						
100 105 110						
CTC ATC CGA ACT TTC CAG CGA CCG GAT CGG GTA GAG CTA GTG CCT CTG	444					
Leu Ile Arg Thr Phe Gln Arg Pro Asp Arg Val Glu Leu Val Pro Leu						
115 120 125						
CCT CCT TGG CAG CCT GTA GGT GAG AAC TTC ACC TTG AGC TGC AGG GTC	492					
Pro Pro Trp Gln Pro Val Gly Glu Asn Phe Thr Leu Ser Cys Arg Val						
130 135 140						
CCG GGG GCA GGA CCC CGA GCG AGC CTC ACA TTG ACC TTG CTG CGA GGC	540					
Pro Gly Ala Gly Pro Arg Ala Ser Leu Thr Leu Thr Leu Leu Arg Gly						
145 150 155 160						

GGC CAG GAG CTG ATT CGC CGA AGT TTC GTA GGC GAG CCA CCC CGA GCT Gly Gln Glu Leu Ile Arg Arg Ser Phe Val Gly Glu Pro Pro Arg Ala 165 170 175	588
CGG GGT GCG ATG CTC ACC GCC ACG GTC CTG GCG CGC AGA GAG GAT CAC Arg Gly Ala Met Leu Thr Ala Thr Val Leu Ala Arg Arg Glu Asp His 180 185 190	636
AGG GCC AAT TTC TCA TGC CTC GCG GAG CTT GAC CTG CGG CCA CAC GGC Arg Ala Asn Phe Ser Cys Leu Thr Ala Glu Leu Asp Leu Arg Pro His Gly 195 200 205	684
TTG GGA CTG TTT GCA AAC AGC TCA GCC CCC AGA CAG CTC CGC ACG TTT Leu Gly Leu Phe Ala Asn Ser Ser Ala Pro Arg Gln Leu Arg Thr Phe 210 215 220	732
GCC ATG CCT CCA CTT TCC CCG AGC CIT ATT GCC CCA CGA TTC TTA GAA Ala Met Pro Pro Leu Ser Pro Ser Leu Ile Ala Pro Arg Phe Leu Glu 225 230 235	780
GTG GGC TCA GAA AGG CCG GTG ACT TGC ACT TTG GAT GGA CTG TTT CCT Val Gly Ser Glu Arg Pro Val Thr Cys Thr Leu Leu Asp Gly Leu Phe Pro 245 250 255	828
GCC CCA GAA GCC GGG GTT TAC CTC TCT CTG GGA GAT CAG AGG CTT CAT Ala Pro Glu Ala Gly Val Tyr Leu Ser Leu Gly Asp Gln Arg Leu His 260 265 270	876
CCT AAT GTG ACC CTC GAC GGG GAG AGC CTT GTG GCC ACT GCC ACA GCT Pro Asn Val Thr Leu Asp Gly Glu Ser Leu Val Ala Thr Ala 275 280 285	924
ACA GCA AGT GAA GAA CAG GAA GGC ACC AAA CAG CTG ATG TGC ATC GTG Thr Ala Ser Glu Glu Gln Glu Gly Thr Lys Gln Leu Met Cys Ile Val 290 295 300	972
ACC CTC GGG GGC GAA AGC AGG GAG ACC CAG GAA AAC CTG ACT GTC TAC Thr Leu Gly Gly Glu Ser Arg Glu Thr Gln Glu Asn Leu Thr Val Tyr 305 310 315	1020
AGC TTC CCG GCT CCT CTT CTG ACT TTA AGT GAG CCA GAA GCC CCC GAG Ser Phe Pro Ala Pro Leu Leu Thr Leu Ser Glu Pro Glu Ala Pro Glu 325 330 335	1068
GGA AAG ATG GTG ACC GTA AGC TGC TGG GCA GGG GCC CGA GCC CTT GTC Gly Lys Met Val Thr Val Ser Cys Trp Ala Ala Gly Ala Arg Ala Leu Val 340 345 350	1116
ACC TTG GAG GGA ATT CCA GCT GCG GTC CCT GGG CAG CCC GCT GAG CTC Thr Leu Glu Gly Ile Pro Ala Ala Val Pro Gly Gln Pro Ala Glu Leu 355 360 365	1164
CAG TTA AAT GTC ACA AAG AAT GAC GAC AAG CGG GGC TTC TTC TGC GAC Gln Leu Asn Val Thr Lys Asn Asp Asp Lys Arg Gly Phe Phe Cys Asp 370 375 380	1212
GCT GCC CTC GAT GTG GAC GGG GAA ACT CTG AGA AAG AAC CAG AGC TCT Ala Ala Leu Asp Val Asp Gly Glu Thr Leu Arg Lys Asn Gln Ser Ser 385 390 400	1260
GAG CTT CGT GTT CTG TAC GCA CCT CGG CTG GAT GAC TTG GAC TGT CCC Glu Leu Arg Val Leu Tyr Ala Pro Arg Arg Asp Asp Leu Asp Cys Pro 405 410 415	1308

AGG AGC TGG ACG TGG CCA GAG GGT CCA GAG CAG ACC CTC CAC TGC GAG Arg Ser Trp Thr 420 Trp Pro Glu Gly Pro Glu Gln Thr Leu His Cys Glu 425	1356
GCC CGT GGA AAC CCT GAG CCC TCC GTG CAC TGT GCA AGG CCT GAC GGT Ala Arg Gly Asn Pro Glu Pro Ser Val His Cys Ala Arg Pro Asp Gly 445	1404
GGG GCG GTG CTA GCG CTG GGC CTG TTG GGT CCA GTG ACC CGT GCC CTC Gly Ala Val Leu Ala Leu Gly Leu Leu Gly Pro Val Thr Thr Ala Leu 450 455 460	1452
GCG GGC ACT TAC CGA TGT ACA GCA ATC AAT GGG CAA GGC CAG GCG GTC Ala Gly Thr Tyr Arg Cys Thr Ala Ile Asn Gly Gln Gly Gln Ala Val 465 470 475 480	1500
AAG GAT GTG ACC CTG ACT GTG GAA TAT GCC CCA GCG CTG GAC AGT GTA Lys Asp Val Thr Thr Val Glu Tyr Ala Pro Ala Leu Asp Ser Val 485 490 495	1548
GGC TGC CCA GAA CGT ATT ACT TGG CTG GAG GGG ACA GAG GCA TCG CTT Gly Cys Pro Glu Arg Ile Thr Trp Leu Glu Gly Thr Glu Ala Ser Leu 500 505 510	1596
AGC TGT GTG GCA CAC GGG GTC CCA CCA CCT AGC GTG AGC TGT GTG GCG Ser Cys Val Ala His Gly Val Pro Pro Ser Val Ser Cys Val Arg 515 520 525	1644
TCT GGA AAG GAG GAA GTC ATG GAA GGG CCC CTG CGT GTG GCC CGG GAG Ser Gly Lys Glu Glu Val Met Glu Gly Pro Leu Arg Val Ala Arg Glu 530 535 540	1692
CAC GCT GGC ACT TAC CGA TGC GAA GCC ATC AAC GCC AGG GGA TCA GCG His Ala Gly Thr Tyr Arg Cys Glu Ala Ile Asn Ala Arg Gly Ser Ala 545 550 555 560	1740
GCC AAA AAT GTG GCT GTC ACG GTG GAA TAT GGT CCC AGT TTT GAG GAG Ala Lys Asn Val Ala Val Thr Val Glu Tyr Gly Pro Ser Phe Glu Glu 565 570 575	1788
TTG GGC TGC CCC AGC AAC TGG ACT TGG GTA GAA GGA TCT GGA AAA CTG Leu Gly Cys Pro Ser Asn Trp Thr Trp Val Glu Gly Ser Gly Lys Leu 580 585 590	1836
TTT TCC TGT GAA GTT GAT GGG AAG CCG GAA CCA CGC GTG GAG TGC GTG Phe Ser Cys Glu Val Asp Gly Lys Pro Glu Pro Arg Val Glu Cys Val 595 600 605	1884
GGC TCG GAG GGT GCA AGC GAA GGG GTA GTG TTG CCC CTG GTG TCC TCG Gly Ser Glu Gly Ala Ser Glu Gly Val Val Leu Pro Leu Val Ser Ser 610 615 620	1932
AAC TCT GGT TCC AGA AAC TCT ATG ACT CCT GGT AAC CTG TCA CCG GGT Asn Ser Gly Ser Arg Asn Ser Met Thr Pro Gly Asn Leu Ser Pro Gly 625 630 635 640	1980
ATT TAC CTC TGC AAC GCC ACC AAC CGG CAT GGC TCC ACA GTC AAA ACA Ile Tyr Leu Cys Asn Ala Thr Asn Arg His Gly Ser Thr Val Lys Thr 645 650 655	2028
GTC GTC GTG AGC GCG GAA TCA CCG CCA CAG ATG GAT GAA TCC AGT TGC Val Val Val Ser Ala Glu Ser Pro Pro Gln Met Asp Glu Ser Cys 660 665 670	2076

CCG AGT CAC CAG ACA TGG CTG GAA GGA GCC GAG GCT ACT GCG CTG GCC Pro Ser His Gln Thr Trp Leu Glu Gly Ala Glu Ala Thr Ala Leu Ala 675 680 685	2124
TGC AGT GCC AGA GGC CGC CCC TCT CCA CGC GTG CGC TGT TCC AGG GAA Cys Ser Ala Arg Gly Arg Pro Ser Pro Arg Val Arg Cys Ser Arg Glu 690 695 700	2172
GGT GCA GCC AGG CTG GAG AGG CTA CAG GTG TCC CGA GAG GAT GCG GGG Gly Ala Ala Arg Leu Glu Arg Leu Gln Val Ser Arg Glu Asp Ala Glu 705 710 715 720	2220
ACC TAC CTG TGT GTG GCT ACC AAC GCG CAT GGC ACG GAT TCA CGG ACC Thr Tyr Leu Cys Val Ala Thr Asn Ala His Gly Thr Asp Ser Arg Thr 725 730 735	2268
GTC ACT GTG GGT GTG GAA TAC CGG CCT GTG GTG GCT GAG CTG GCA GCC Val Thr Val Gly Val Glu Tyr Arg Pro Val Val Ala Glu Leu Ala Ala 740 745 750	2316
TCG CCC CCA AGC GTG CGG CCT GGC GGA AAC TTC ACT CTG ACC TGC CGT Ser Pro Pro Ser Val Arg Pro Gly Gly Asn Phe Thr Leu Thr Cys Arg 755 760 765	2364
GCA GAG GCC TGG CCT CCA GCC CAG ATC AGC TGG CGC GCG CCC CCG GGA Ala Glu Ala Trp Pro Pro Ala Gln Ile Ser Trp Arg Ala Pro Pro Gly 770 775 780	2412
GCT CTC AAC CTC GGT CTC TCC AGC AAC AAC AGC ACG CTG AGC GTG GCG Ala Leu Asn Leu Gly Leu Ser Ser Asn Asn Ser Thr Leu Ser Val Ala 785 790 795 800	2460
GGT GCC ATG GGC AGC CAT GGT GGC GAG TAT GAG TGC GCA GCC ACC AAT Gly Ala Met Gly Ser His Gly Gly Glu Tyr Glu Cys Ala Ala Thr Asn 805 810 815	2508
GCG CAT GGG CGC CAC GCA CGG CGC ATC ACG GTG CGC GTG GCC GGT CCA Ala His Gly Arg His Ala Arg Arg Ile Thr Val Arg Val Ala Gly Pro 820 825 830	2556
TGG CTG TGG GTC GCT GTG GGC GGT GCG GCA GGG GGC GCG GCG CTG CTG Trp Leu Trp Val Ala Val Gly Gly Ala Ala Gly Gly Ala Ala Leu Leu 835 840 845	2604
GCC GCA GGG GCC GGC CTG GCC TTC TAC GTG CAG TCC ACC GCT TGC AAG Ala Ala Gly Ala Gly Leu Ala Phe Tyr Val Gln Ser Thr Ala Cys Lys 850 855 860	2652
AAG GGA GAG TAC AAC GTC CAG GAG GCT GAG AGC TCA GGC GAG GCG GTG Lys Gly Glu Tyr Asn Val Gln Glu Ala Glu Ser Ser Gly Glu Ala Val 865 870 875 880	2700
TGT CTC AAT GGC GCG GGC GGG ACA CCG GGT GCA GAA GGC GGA GCA GAG Cys Leu Asn Gly Ala Gly Gly Thr Pro Gly Ala Glu Gly Gly Ala Glu 885 890 895	2748
ACC CCC GGC ACT GCC GAG TCA CCT GCA GAT GGC GAG GIT TTC GCC ATC Thr Pro Gly Thr Ala Glu Ser Pro Ala Asp Gly Glu Val Phe Ala Ile 900 905 910	2796
CAG CTG ACA TCT TCC TGAGCCTGTA TCCAGCTCCC CCAGGGGCGCT CGAAGCACCA Gln Leu Thr Ser Ser 915	2851

GGGGTGGACG TATGTATTGT TCACTCTCTA TTTATTCAAC TCCAGGGGCG TCGTCCCCGT 2911
 TTCTACCCA TTCCCTTAAT AAAGTTTTA TAGGAGAAAA AAAAAAAAAA AAAAAAAAAA 2971
 AAAAAAAAAA AAAAAA 2988

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 917 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Pro	Gly	Pro	Ser	Pro	Gly	Leu	Arg	Arg	Thr	Leu	Leu	Gly	Leu	Trp
1			5					10						15	
Ala	Ala	Leu	Gly	Leu	Gly	Ile	Leu	Gly	Ile	Ser	Ala	Val	Ala	Leu	Glu
			20					25					30		
Pro	Phe	Trp	Ala	Asp	Leu	Gln	Pro	Arg	Val	Ala	Leu	Val	Glu	Arg	Gly
		35						40				45			
Gly	Ser	Leu	Trp	Leu	Asn	Cys	Ser	Thr	Asn	Cys	Pro	Arg	Pro	Glu	Arg
		50				55					60				
Gly	Gly	Leu	Glu	Thr	Ser	Leu	Arg	Arg	Asn	Gly	Thr	Gln	Arg	Gly	Leu
65					70					75					80
Arg	Trp	Leu	Ala	Arg	Gln	Leu	Val	Asp	Ile	Arg	Glu	Pro	Glu	Thr	Gln
				85					90					95	
Pro	Val	Cys	Phe	Arg	Cys	Ala	Arg	Arg	Thr	Leu	Gln	Ala	Arg	Gly	
		100					105					110			
Leu	Ile	Arg	Thr	Phe	Gln	Arg	Pro	Asp	Arg	Val	Glu	Leu	Val	Pro	Leu
		115				120					125				
Pro	Pro	Trp	Gln	Pro	Val	Gly	Glu	Asn	Phe	Thr	Leu	Ser	Cys	Arg	Val
		130				135					140				
Pro	Gly	Ala	Gly	Pro	Arg	Ala	Ser	Leu	Thr	Leu	Thr	Leu	Leu	Arg	Gly
145					150				155					160	
Gly	Gln	Glu	Leu	Ile	Arg	Arg	Ser	Phe	Val	Gly	Glu	Pro	Pro	Arg	Ala
			165						170					175	
Arg	Gly	Ala	Met	Leu	Thr	Ala	Thr	Val	Leu	Ala	Arg	Arg	Glu	Asp	His
			180					185					190		
Arg	Ala	Asn	Phe	Ser	Cys	Leu	Ala	Glu	Leu	Asp	Leu	Arg	Pro	His	Gly
		195				200						205			
Leu	Gly	Leu	Phe	Ala	Asn	Ser	Ser	Ala	Pro	Arg	Gln	Leu	Arg	Thr	Phe
		210				215					220				
Ala	Met	Pro	Pro	Leu	Ser	Pro	Ser	Leu	Ile	Ala	Pro	Arg	Phe	Leu	Glu
225					230					235					240

Val Gly Ser Glu Arg Pro Val Thr Cys Thr Leu Asp Gly Leu Phe Pro	245	250	255
Ala Pro Glu Ala Gly Val Tyr Leu Ser Leu Gly Asp Gln Arg Leu His	260	265	270
Pro Asn Val Thr Leu Asp Gly Glu Ser Leu Val Ala Thr Ala Thr Ala	275	280	285
Thr Ala Ser Glu Glu Gln Glu Gly Thr Lys Gln Leu Met Cys Ile Val	290	295	300
Thr Leu Gly Gly Glu Ser Arg Glu Thr Gln Glu Asn Leu Thr Val Tyr	305	310	315
Ser Phe Pro Ala Pro Leu Leu Thr Leu Ser Glu Pro Glu Ala Pro Glu	325	330	335
Gly Lys Met Val Thr Val Ser Cys Trp Ala Gly Ala Arg Ala Leu Val	340	345	350
Thr Leu Glu Gly Ile Pro Ala Ala Val Pro Gly Gln Pro Ala Glu Leu	355	360	365
Gln Leu Asn Val Thr Lys Asn Asp Asp Lys Arg Gly Phe Phe Cys Asp	370	375	380
Ala Ala Leu Asp Val Asp Gly Glu Thr Leu Arg Lys Asn Gln Ser Ser	385	390	395
Glu Leu Arg Val Leu Tyr Ala Pro Arg Leu Asp Asp Leu Asp Cys Pro	405	410	415
Arg Ser Trp Thr Trp Pro Glu Gly Pro Glu Gln Thr Leu His Cys Glu	420	425	430
Ala Arg Gly Asn Pro Glu Pro Ser Val His Cys Ala Arg Pro Asp Gly	435	440	445
Gly Ala Val Leu Ala Leu Gly Leu Leu Gly Pro Val Thr Arg Ala Leu	450	455	460
Ala Gly Thr Tyr Arg Cys Thr Ala Ile Asn Gly Gln Gly Gln Ala Val	465	470	475
Lys Asp Val Thr Leu Thr Val Glu Tyr Ala Pro Ala Leu Asp Ser Val	485	490	495
Gly Cys Pro Glu Arg Ile Thr Trp Leu Glu Gly Thr Glu Ala Ser Leu	500	505	510
Ser Cys Val Ala His Gly Val Pro Pro Pro Ser Val Ser Cys Val Arg	515	520	525
Ser Gly Lys Glu Glu Val Met Glu Gly Pro Leu Arg Val Ala Arg Glu	530	535	540
His Ala Gly Thr Tyr Arg Cys Glu Ala Ile Asn Ala Arg Gly Ser Ala	545	550	555
Ala Lys Asn Val Ala Val Thr Val Glu Tyr Gly Pro Ser Phe Glu Glu	565	570	575

Leu	Gly	Cys	Pro	Ser	Asn	Trp	Thr	Trp	Val	Glu	Gly	Ser	Gly	Lys	Leu
			580					585					590		
Phe	Ser	Cys	Glu	Val	Asp	Gly	Lys	Pro	Glu	Pro	Arg	Val	Glu	Cys	Val
		595					600					605			
Gly	Ser	Glu	Gly	Ala	Ser	Glu	Gly	Val	Val	Leu	Pro	Leu	Val	Ser	Ser
		610				615						620			
Asn	Ser	Gly	Ser	Arg	Asn	Ser	Met	Thr	Pro	Gly	Asn	Leu	Ser	Pro	Gly
					630					635					640
Ile	Tyr	Leu	Cys	Asn	Ala	Thr	Asn	Arg	His	Gly	Ser	Thr	Val	Lys	Thr
				645					650					655	
Val	Val	Val	Ser	Ala	Glu	Ser	Pro	Pro	Gln	Met	Asp	Glu	Ser	Ser	Cys
				660					665					670	
Pro	Ser	His	Gln	Thr	Trp	Leu	Glu	Gly	Ala	Glu	Ala	Thr	Ala	Leu	Ala
				675				680					685		
Cys	Ser	Ala	Arg	Gly	Arg	Pro	Ser	Pro	Arg	Val	Arg	Cys	Ser	Arg	Glu
		690				695					700				
Gly	Ala	Ala	Arg	Leu	Glu	Arg	Leu	Gln	Val	Ser	Arg	Glu	Asp	Ala	Gly
	705				710						715				720
Thr	Tyr	Leu	Cys	Val	Ala	Thr	Asn	Ala	His	Gly	Thr	Asp	Ser	Arg	Thr
				725					730					735	
Val	Thr	Val	Gly	Val	Glu	Tyr	Arg	Pro	Val	Val	Ala	Glu	Leu	Ala	Ala
			740					745					750		
Ser	Pro	Pro	Ser	Val	Arg	Pro	Gly	Gly	Asn	Phe	Thr	Leu	Thr	Cys	Arg
			755				760					765			
Ala	Glu	Ala	Trp	Pro	Pro	Ala	Gln	Ile	Ser	Trp	Arg	Ala	Pro	Pro	Gly
			770			775					780				
Ala	Leu	Asn	Leu	Gly	Leu	Ser	Ser	Asn	Asn	Ser	Thr	Leu	Ser	Val	Ala
					790					795					800
Gly	Ala	Met	Gly	Ser	His	Gly	Gly	Glu	Tyr	Glu	Cys	Ala	Ala	Thr	Asn
				805					810					815	
Ala	His	Gly	Arg	His	Ala	Arg	Arg	Ile	Thr	Val	Arg	Val	Ala	Gly	Pro
				820				825						830	
Trp	Leu	Trp	Val	Ala	Val	Gly	Gly	Ala	Ala	Gly	Gly	Ala	Ala	Leu	Leu
				835			840					845			
Ala	Ala	Gly	Ala	Gly	Leu	Ala	Phe	Tyr	Val	Gln	Ser	Thr	Ala	Cys	Lys
						855					860				
Lys	Gly	Glu	Tyr	Asn	Val	Gln	Glu	Ala	Glu	Ser	Ser	Gly	Glu	Ala	Val
					870					875					880
Cys	Leu	Asn	Gly	Ala	Gly	Gly	Thr	Pro	Gly	Ala	Glu	Gly	Gly	Ala	Glu
				885					890					895	
Thr	Pro	Gly	Thr	Ala	Glu	Ser	Pro	Ala	Asp	Gly	Glu	Val	Phe	Ala	Ile
				900				905					910		

Gln Leu Thr Ser Ser
915

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCG GAT CGG GTA GAG CTA GTG CCT CTG CCT CCT TGG CAG CCT GTA GGT	48
Pro Asp Arg Val Glu Leu Val Pro Leu Pro Pro Trp Gln Pro Val Gly	
1 5 10 15	
GAG AAC TTC ACC TTG AGC TGC AGG GTC CCG GGG GCA GGA CCC CGA GCG	96
Glu Asn Phe Thr Leu Ser Cys Arg Val Pro Gly Ala Gly Pro Arg Ala	
20 25 30	
AGC CTC ACA TTG ACC TTG CTG CGA GGC GGA CAG GAG CTG ATT CGC CGA	144
Ser Leu Thr Leu Thr Leu Leu Arg Gly Gly Gln Leu Ile Arg Arg	
35 40 45	
AGT TTC GTA GGC GAG CCA CCC CGA GCT CGG TGT GCG ATG CTC ACC GCC	192
Ser Phe Val Gly Glu Pro Pro Arg Ala Arg Cys Ala Met Leu Thr Ala	
50 55 60	
ACG GTC CTG GCG CGC AGA GAG GAT CAC AGG GAC AAT TTC TCA TGC CTC	240
Thr Val Leu Ala Arg Arg Glu Asp His Arg Asp Asn Phe Ser Cys Leu	
65 70 75 80	
GCG GAG CIT GAC CTG CGG ACA CAC GGC TTG GGA CTG TTT GCA AAC AGC	288
Ala Glu Leu Asp Leu Arg Thr His Gly Leu Gly Leu Phe Ala Asn Ser	
85 90 95	
TCA GCC CCC AGA CAG CTC CGC ACG TTT	315
Ser Ala Pro Arg Gln Leu Arg Thr Phe	
100 105	

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1781 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 16..1659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGCTCTCTG TCAGA	ATG GCC ACC ATG GTA CCA TCC GTG TTG TGG CCC AGG	51
Met Ala Thr Met Val Pro Ser Val Leu Trp Pro Arg	1 5 10	
GCC TGC TGG ACT CTG CTG GTC TGC TGT CTG CTG ACC CCA GGT GTC CAG	Ala Cys Trp Thr Leu Leu Val Cys Leu Leu Thr Pro Gly Val Gln	99
15 20 25		
GGG CAG GAG TTC CTT TTG CGG GTG GAG CCC CAG AAC CCT GTG CTC TCT	Gly Gln Glu Phe Leu Leu Arg Val Glu Pro Gln Asn Pro Val Leu Ser	147
30 35 40		
GCT GGA GGG TCC CTG TTT GTG AAC TGC AGT ACT GAT TGT CCC AGC TCT	Ala Gly Gly Ser Leu Phe Val Asn Cys Ser Thr Asp Cys Pro Ser Ser	195
45 50 55 60		
GAG AAA ATC GCC TTG GAG ACG TCC CTA TCA AAG GAG CTG GTG GCC AGT	Glu Lys Ile Ala Leu Glu Thr Ser Leu Ser Lys Glu Leu Val Ala Ser	243
65 70 75		
GGC ATG GGC TGG GCA GCC TTC AAT CTC AGC AAC GTG ACT GGC AAC AGT	Gly Met Gly Trp Ala Ala Phe Asn Leu Ser Asn Val Thr Gly Asn Ser	291
80 85 90		
CGG ATC CTC TGC TCA GTG TAC TGC AAT GGC TCC CAG ATA ACA GGC TCC	Arg Ile Leu Cys Ser Val Tyr Cys Asn Gly Ser Gln Ile Thr Gly Ser	339
95 100 105		
TCT AAC ATC ACC GTG TAC GGG CTC CCG GAG CGT GTG GAG CTG GCA CCC	Ser Asn Ile Thr Val Tyr Gly Leu Pro Glu Arg Val Glu Leu Ala Pro	387
110 115 120		
CTG CCT CCT TGG CAG CCG GTG GGC CAG AAC TTC ACC CTG CGC TGC CAA	Leu Pro Pro Trp Gln Pro Val Gly Gln Asn Phe Thr Leu Arg Cys Gln	435
125 130 135 140		
GTG GAG GGT GGG TCG CCC CGG ACC AGC CTC ACG GTG GTG CTG CTT CGC	Val Glu Gly Gly Ser Pro Arg Thr Ser Leu Thr Val Val Leu Leu Arg	483
145 150 155		
TGG GAG GAG GAG CTG AGC CGG CAG CCC GCA GTG GAG GAG CCA GCG GAG	Trp Glu Glu Glu Leu Ser Arg Gln Pro Ala Val Glu Glu Pro Ala Glu	531
160 165 170		
GTC ACT GCC ACT GTG CTG GCC AGC AGA GAC GAC CAC GGA GCC CCT TTC	Val Thr Ala Thr Val Leu Ala Ser Arg Asp Asp His Gly Ala Pro Phe	579
175 180 185		
TCA TGC CGC ACA GAA CTG GAC ATG CAG CCC CAG GGG CTG GGA CTG TTC	Ser Cys Arg Thr Glu Leu Asp Met Gln Pro Gln Gly Leu Gly Leu Phe	627
190 195 200		
GTG AAC ACC TCA GCC CCC CGC CAG CTC CGA ACC TTT GTC CTG CCC GTG	Val Asn Thr Ser Ala Pro Arg Gln Leu Arg Thr Phe Val Leu Pro Val	675
205 210 215 220		
ACC CCC CGC CGC CTC GTG GCC CCC CGG TTC TTG GAG GTG GAA ACG TCG	Thr Pro Pro Arg Leu Val Ala Pro Arg Phe Leu Glu Val Glu Thr Ser	723
225 230 235		
TGG CCG GTG GAC TGC ACC CTA GAC GGG CTT TTT CCA GCC TCA GAG GCC	Trp Pro Val Asp Cys Thr Leu Asp Gly Leu Phe Pro Ala Ser Glu Ala	771
240 245 250		

CAG GTC TAC CTG GCG CTG GGG GAC CAG ATG CTG AAT GCG ACA GTC ATG Gln Val Tyr 255 Leu Ala Leu Gly Asp 260 Gln Met Leu Asn 265 Ala Thr Val Met	819
AAC CAC GGG GAC ACG CTA ACG GCC ACA GCC ACA GCC ACG GCG CGC GCG Asn His Gly Asp Thr Leu Thr 275 Ala Thr 280 Ala Thr Ala Arg Ala	867
GAT CAG GAG GGT GCC CGG GAG ATC GTC TGC AAC GTG ACC CTA GGG GGC Asp Gln Glu Gly Ala 290 Glu Ile Val Cys Asn 295 Val Thr Leu Gly 300	915
GAG AGA CGG GAG GCC CGG GAG AAC TTG ACG GTC TTT AGC TTC CTA GGA Glu Arg Arg Glu 305 Arg Glu Asn Leu Thr Val Phe Ser Phe Leu Gly 315	963
CCC ATT GTG AAC CTC AGC GAG CCC ACC GCC CAT GAG GGG TCC ACA GTG Pro Ile Val Asn 320 Leu Ser Glu Pro 325 Thr Ala His Glu Gly 330 Thr Val	1011
ACC GTG AGT TGC ATG GCT GGG GCT CGA GTC CAG GTC ACG CTG GAC GGA Thr Val Ser Cys Met Ala Gly 335 Ala Arg Val Gln Val Thr Leu Asp Gly	1059
GTT CCG GCC GCG GCC CCG GGG CAG ACA GCT CAA CTT CAG CTA AAT GCT Val Pro Ala Ala Ala Pro Gly 350 Gln Thr Ala Gln Leu Gln Leu Asn Ala	1107
ACC GAG AGT GAC GAC GGA CGC AGC TTC TTC TGC AGT GCC ACT CTC GAG Thr Glu Ser Asp Asp Gly 365 Arg Ser Phe Phe Cys Ser Ala Thr Leu Glu 380	1155
GTG GAC GGC GAG TTC TTG CAC AGG AAC AGT AGC GTC CAG CTG CGA GTC Val Asp Gly Glu Phe 385 Leu His Arg Asn Ser Ser Val Gln Leu Arg Val 395	1203
CTG TAT GGT CCC AAA ATT GAC CGA GCC ACA TGC CCC CAG CAC TTG AAA Leu Tyr Gly Pro Lys Ile Asp Arg Ala Thr Cys Pro Gln His Leu Lys 400 405 410	1251
TGG AAA GAT AAA ACG AGA CAC GTC CTG CAG TGC CAA GCC AGG GGC AAC Trp Lys Asp Lys Thr Arg His Val Leu Gln Cys Gln Ala Arg Gly Asn 415 420 425	1299
CCG TAC CCC GAG CTG CGG TGT TTG AAG GAA GGC TCC AGC CGG GAG GTG Pro Tyr Pro Pro Glu Arg Cys Leu Lys Glu Gly 430 435 440 440 440 440	1347
CCG GTG GGG ATC CCG TTC TTC GTC AAC GTA ACA CAT AAT GGT ACT TAT Pro Val Gly Ile Pro Phe Val Asn Val Thr 445 450 455 455 460 460	1395
CAG TGC CAA GCG TCC AGC TCA CGA GGC AAA TAC ACC CTG GTC GTG GTG Gln Cys Gln Ala Ser Ser Ser Arg Gly 465 470 475 475 475 475	1443
ATG GAC ATT GAG GCT GGG AGC TCC CAC TTT GTC CCC GTC TTC GTG GCG Met Asp Ile Glu Ala Gly Ser Ser His Phe Val Pro Val Phe Val Ala 480 485 490 490 490 490	1491
GTG TTA CTG ACC CTG GGC GTG GTG ACT ATC GTA CTG GCC TTA ATG TAC Val Leu Leu Thr Leu Gly Val Val Thr Ile Val Leu Ala Leu Met Tyr 495 500 505 505 505 505	1539

GTC TTC AGG GAG CAC CAA CGG AGC GGC AGT TAC CAT GTT AGG GAG GAG	1587
Val Phe Arg Glu His Gln Arg Ser Gly Ser Tyr His Val Arg Glu Glu	
510 515 520	

AGC ACC TAT CTG CCC CTC ACG TCT ATG CAG CCG ACA GAA GCA ATG GGG	1635
Ser Thr Tyr Leu Pro Leu Thr Ser Met Gln Pro Thr Glu Ala Met Gly	
525 530 535 540	

GAA GAA CCG TCC AGA GCT GAG TGACGCTGGG ATCCGGGATC AAAGTTGGCG	1686
Glu Glu Pro Ser Arg Ala Glu	
545	

GGGGCTTGGC TGTGCCCTCA GATTCCGCAC CAATAAGGCC TTCAACTCC CAAAAAAAAA	1746
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AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAA	1781
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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGAACGCTC CTCGCCCTCT GGTCNCTCTT GGNCTCGGGG ATCCTAGGCA TCTCAGGTAA	60
GAAGAGCCCG CCCGTGGAGC NAGGTGGATA AGGCGGGGGC GGAATTGAAG GACCAGAGAG	120
GGCGGCCCGG GTGTCCCCCT CCAGGCTCCG CCTCTTCTA GCTTCCCACG CTTCTGTAC	180
CACCTGGAGN TCGGGGGCTTC TCCCCGTCTT TCCTCCACCC CAACACACCT CAATCTTTCA	240
GANCTGAACC CAGCACCTTT TCTGGANING GGGNNTTGCA CCTAACCTGT CTCAGGAGAN	300
ACTGTGGCTC TCCTGTCTCT TCCTGCTCTG TNATGCCCTA TGGTTCACAG ACTGGCATCA	360
TCCTTATTCA TGATCCTCAA AGACNCCATC TCCTCAACTG TCATAACTCA GAGCTCTATT	420
CCCCCTCCAC CTGGAGCCCT GGAACCCGGC TTTCTAGGGC TTTTCTCCCG GGTCTTTTCC	480
CGGAGTTCAG CGTTGTGGCT TTTTGTCCAA GTTACTCAAG TTTGGGGACA ATCTCCTTTA	540
AGCCITTTGAC TCAGTCTCAT TTCCACTTTG CTTTGTCCCC AAGCCTCTGT GTCTCTCCCC	600
CATTTCTCTGA CGATCTGTCA GAGTCTTAAG AGTGATTGAG TTCCCCATCC CCCCTCCAAC	660
TGGAGTCTCT TCCTCACTAT TGATGTGTGC ATCTGAGACC CCCATCCCCG CACCGAGTTT	720
CCCCATCTCT GTCACTAAAG AGCAAGGCTT CCAGAGACAA CCTCTAATA GCGCGTCAGT	780
CCCGAATCTT GAGTGGGATG GGGGACTCCC GTGCTATTTC TTGGCGGAGG TCTTTCTTGG	840
TCCTTATGGA CACCCTGGT TTGGGATATG GGGGCCGCTA AGATTTCAGA GATGGGGTCC	900
CTAGGCTGAG NCCCGTTTTT CCCGGGCAGC GGTCTCGCTA GAACCTTTCT GGGCGGACCT	960
TCAGCCCCCG GTGGCGCTCG TGGAGCGCGG GGGCTCGCTG TGCTCTCACT GCAGCACTAA	1020
CTGTCCGAGG CCGGAGCGCG GTGGCCTGGA GACCTCGCTA CGCCGAAACG GGACCCAGAG	1080

GGGTCTGNAC	TGNTGGCTC	GACAGCTGGT	GGACATCCGA	GANCTGAAA	CCCAGCCGGT	1140
CTGCTTCTTC	CNCTGCGCG	GCCGCACACT	CCAAGCGCGT	GGGCTCATCC	GAACCTTCCG	1200
TGAGTTCAGG	GTGGGCACNC	CCCTTGGGTC	TCTGGACCTC	CCCCTCAAGC	TCCTCCACC	1260
CGCCCTCTGA	TCCTCCTGCT	TGTTCTGAAA	GTACTACAGC	TGGCTAGAGC	GGAGTTTTTG	1320
GTCCCTTGCA	GAGCGACCG	ATCGGCTAGA	GCTAGTGCCT	CTGCCTCCIT	GGCAGCCTGT	1380
AGGTGAGAAC	TTACCTTGA	GCTGCAGGGT	CCCGGGGGCA	GGACCCCGAG	CGAGCCTCAC	1440
ATTGACCTTG	CTGCGAGGCG	GCCAGGAGCT	GATTCGCCGA	AGTTTCGTAG	GCGAGCCACC	1500
CCGAGCTCGG	GGTGCGATGC	TCACCGCCAC	GGTCCTGGCG	CGCAGAGAGG	ATCACAGGGC	1560
CAATTTCTCA	TGCTTCGCG	AGCTTGACCT	GCGNCCACAC	GGCTTGGGAC	TGTTTGCA	1620
CAGCTCAGCC	CCCAGACAGC	TCCGCACGTT	TGGTGAGTGT	GGACCTTAAC	TGACAGATTT	1680
TAAGAAGTTT	AGGGCAGCCA	GGCGTGTTGG	CATGGTGTG	TAGGCCCTAA	GTCCAGCCCC	1740
AAGCAGANCT	AAGNCGGATC	TCTTGTGAAT	TAAAAGTCTA	GCTCGTCTAC	ATAACGAGGN	1800
CTGCATAGTT	AAATCCCCCA	AAAGTCTAAG	CAGCTAGCCC	TTACTTCCAA	CACAAGTACT	1860
AGCTTAAGTA	CTTTCTCCTG	TGAGCTTTTT	CCTTTATGTA	TTTACTCGTT	GAGAGAAAAA	1920
GAGAGTGTGT	GTACGTGCCT	TTATGCACAT	GCCGCAGTGC	TGTATGGA	GTTAAAGAAT	1980
AAGGAGGCGT	TCTGCCCTTC	CATCCTGTGG	GTCTAGGGG	TGTTATTAGC	TCCTCAGGCT	2040
TTGTTAGTNA	CAAGCGCCTA	GGCTTGGGGA	GCCATCTCGC	CCGCTCCTCT	GTATCTTTAG	2100
GGTGAAACCA	GACAAATGCAT	GCAAATTGGT	TGATCAACAC	TGAATGTTTA	GTTCTGTAAT	2160
TCAAGCTCTG	TTCTTTGTCT	TCCTCAGCCA	TGCTTCCACT	TTCCCCCGAG	CCTTATTGCC	2220
CCACGATTCT	TAGAAGTGGG	CTCAGAAAGG	CCGGTGACKT	GCACTTTGGA	TGGACTGTTT	2280
CCTGCCCCAG	AAGCCGGGGT	TTACTTCTCT	CTGGGAGATC	AGAGGCTTCA	TCCTAATGTG	2340
ACCTTCGACG	GGGAGAGCCT	TGTGGCCACT	GCCACAGCTA	CAGCAAGTGA	AGAACAGGAA	2400
GGCACCAAAAC	AGCTGATGTG	CATCGTGACC	CTCGGGGGCG	AAAGCAGGGA	GACCCAGGAA	2460
AACCTGACTG	TCTACAGTAA	GGGGAATCCA	ACAAGACCTT	CAATAGCTCA	GACTGGGGCT	2520
GGGGCTGGGT	CTGGGTCTGG	GGCCAGAGTC	TCACAAAGGC	GGAGCCTATA	AAGTGGGCGG	2580
GACCTCCACA	CCAGAAACAG	CCGGGCGGGA	GAGTTCAGG	GCAGGAGCAG	ATAGAAGTTG	2640
GAAATTAATA	GATTGGGTTG	AGTTCCTCTGA	GTGGGGAGTG	AACCCCAACC	AATTCTCTGT	2700
CCCCAGGCTT	CCCGGCTCCT	CTTCTGACTT	TAAGTGAGCC	AGAAGCCCCC	GAGGGAAAGA	2760
TGGTGACCGT	AAGCTGCTGG	GCGAGGGGCC	GAGCCCTTGT	CACCTTGAGG	GGAATTCCAA	2820
GGACCCTCTT	ACCGGCCCCA	TCTTTAACCT	TATCGTATCC	CCTCTGCCTC	ATGCCCGCAG	2880
ACGCACCTCG	GCTGGATGAC	TTGGACTGTC	CCAGGAGCTG	GACGTGGCCA	GAGGGTCCAG	2940
AGCAGACCTT	CCACTGCGAG	GCCCGTGGAA	ACCCTGAGCC	CTCCGTGCAC	TGTGCAAGGC	3000

CTGACGGTGG	GGCGGTGCTA	GCCTGGGGCC	TGTTGGGTCC	AGTGACCCGT	GCCCTCGCGG	3060
GCACCTTACCG	ATGTACAGCA	ATCAATGGGC	AAGGCCAGGC	GGTCAAGGAT	GTGACCCTGA	3120
CTGTGGAATG	TGAGTAGGGG	GAGGTGGGCA	TGCTTATCCC	TTTAAGGTCA	CGGAGTGATC	3180
TGGGAGACTG	GCTATACGGA	AAGGAAGAA	GCCTAGGTTT	AGCAGGGATT	GGGAAAACAC	3240
TGAAGGAAAG	TGGTGTGGTG	TTTACAACT	TAACGGTGGT	AACTGGGCAC	GGTCTGGCAA	3300
AAACAGACAG	CCAAGAGAGT	GTGCCTGGGA	AGCTGCAATG	GGGGCTTTGT	GGGAATTGGT	3360
CAACAGCACC	CTGAGATCTC	AGGAAAGGGG	CCTGAAGTTA	TCTCCAGAAC	CCATGTGAAG	3420
GCAGGAAGAG	AGAACGCCCA	CCTTTTCCTG	CTCCCCCCAA	CCCCCCCCCA	CATATCACAC	3480
GGAGTATATA	AATAAATAAA	ATGGCTCCTG	CCGGAGGGAG	TGAGAAGCTG	TCTCCTGCAG	3540
GCTCAGAGCA	GTGGTAGTGC	ATGCCTTTAA	TCCCAGCACT	CGGTAGGCAA	AGGCAGGCAG	3600
ATCTCTGTGA	ATGTGGGGCC	AGCCTGGTCT	GTACAGAGAA	ATCCTGTCTC	AAAACAAACC	3660
AGCAAAGAAA	CAAAACCAAA	ATCAATTCCA	GATGCCCCAG	CGCTGGACAG	TGTAGGCTGC	3720
CCANGACGTA	TTACTTGNCT	GGAGGGGACA	GAGGCATCGC	TTAGCTGTGT	GGCACACGGG	3780
GTCCCAACCAC	CTAGCGTGAG	CTGTGTGCGC	TCTGAAAGG	AGGAAGTCAT	GGAAGGGCCC	3840
CTGCGTGTGG	CCCGGGAGCA	CGCTGGCACT	TACCGATGCG	AAGCCATCAA	CGCCAGGGGA	3900
TCAGCGGNCA	AAAATGTGGC	TGTCACGGTG	GAATGTGAGT	AGGGGTGGCT	ACGGAATGT	3960
CCACACCTGC	GTCTCTGTGC	CTCAGTGTGA	ACTCCTATTT	CCCTGCTTCC	TAGATGGTCC	4020
CAGTTTNTGAG	GAGTTGGGCT	GCCCCAGCAA	CTGGACTTGG	GTAGAAGGAT	CTGGAAAACT	4080
GTTTTCTGTG	GAGTTGATG	GGAAGCCGGA	ACCACGCGTG	GAGTGCCTGG	GCTCGGAGGG	4140
TGCAAGCGAA	GGGGTAGTGT	TGCCCCCTGGT	GTCTCTGAAC	TCTGGTTCCA	GAACCTCTAT	4200
GACTCTGGT	AACCTGTCA	CGGGTATTTA	CCTCTGCAAC	GCCACCAACC	GGCATGGCTC	4260
CACAGTCAAA	ACAGTCGTGC	TGAGCGCGGA	ATGTGAGCAG	GGGCCAGGT	GGCGGAGAG	4320
TACCGGGTGT	CCCAGGATCT	TTTCTTTCCC	TGATGCCCTT	CCTTATGGTG	GCTGATCTGC	4380
AGCACGCGCA	CAGATGGATG	AATCCAGTTG	CCCGAGTCAC	CAGACATGGC	TGGAAGGAGC	4440
CGAGGCTACT	GCCTGGGCT	GCAGTGACAG	GGGNCGCCCC	TCTCCAGCGC	TGCGCTGTTC	4500
CAGGGAAGGT	GCAGCCAGGC	TGGAGAGGCT	ACAGGTGTCC	CGAGAGGATG	CGGGGACCTA	4560
CCTGTGTGTG	GCTACCAACG	CGCATGGCAC	GGATTCACGG	ACCCTCACTG	TGGGTGTGGA	4620
ATGTGAGTGA	GGACAGCGCT	GAATGAAGAC	GACTCAGACC	GCCAGAAAAG	TGCCTTGAGG	4680
CCTGGGATGT	ATGATCCAGT	GGGTAGAGTG	CTCAATTAGC	ACTCACTAAA	ATGTATATTTC	4740
TATTCTTAAT	ACTCTTTAAT	TTTANCTTTT	GGGAGGCAGA	GACAGGCAGA	TCTCTGTTCC	4800
GGGATAACCT	GCTCTCTGTC	TAGGACAGCT	TGGTCTACAG	AGGGGNTACA	GGCCCCCCTT	4860
CCCAAGATTG	NATAGCAACC	CTCTGGCTCC	CTGTCTCTCT			4900

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1295 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

NGAATTC	CGGATCGGGT	AGAGCTAGTG	CCTCTGCCTC	CTTGGCAGCC	TGTAGGTGAG	60
AAC	TTACACCT	TGAGCTGCAG	GGTCCCGGGG	GCAGGACCCC	GAGCGAGCCT	120
TTGCTG	CGGAG	GCTGATTCGC	CGAAGTTTCG	TAGGCGAGCC	ACCCCGAGCT	180
CGGGGTG	CGA	TGCTCACCGC	CACGCTCCTG	GCGCGCAGAG	AGGATCACAG	240
TCATGCT	CGC	GAGCTTGA	CCTGCGGCCA	CACGGCTTGG	GACTGTTTGC	300
GCCCCAG	CAG	AGCTCCGCAC	GTTTGCCATG	CCTCCACTTT	CCCCGAGCCT	360
CGATTCT	TAG	AAGTGGGCTC	AGAAAAGCCG	GTGACTTGCA	CTTTGGATGG	420
GCCCCAGA	AG	CGGGGTTTA	CCTCTCTCTG	GGAGATCAGA	GGCTTATATC	480
CTCGACG	GGG	AGAGCCTTGT	GGCCACTGCC	ACAGCTACAG	CAAGTGAAGA	540
ACCAAA	CAGC	TGATGTGCAT	CGTGACCCTC	GGGGGCGAAA	GCAGGGAGAC	600
CTGACTGT	CT	ACAGCTTCCC	GGCTCCTCTT	CTGACTTTAA	GTGAGCCAGA	660
GGAAAGAT	G	TGACCGTAAG	CTGCTGGGCA	GGGGCCCGAG	CCCTTGTCAC	720
ATTCCA	AGGA	CCCTCTTACC	GGCCCCATCT	TTAACCTTAT	CGTATCCCTC	780
CCGCGA	GACG	CACCTCGGCT	GGATGACTTG	GACTGTCCCA	GGAGCTGGAC	840
GGTCCAG	AGC	AGACCTCCA	CTGCGAGGCC	CGTGGAAACC	CTGAGCCCTC	900
GCAAGCC	CTG	ACGGTGGGGC	GGTGCTAGCG	CTGGGCTGT	TGGGTCCAGT	960
CTCGCG	GGA	CTTACCGATG	TACAGCAATC	AATGGGCAAG	GCCAGGCGGT	1020
ACCTG	GA	CTG	GAATATGC	CCCAGCGCTG	GACAGTGTAG	1080
TGGCTG	AGG	GGACAGAGGC	ATCGCTTAGC	TGTGTGGCAC	ACGGGGTCCC	1140
GTGAGCT	GTG	TGCGCTCTGG	AAAGGAGGAA	GTCATGGAAG	GGCCCTTGCG	1200
GAGCAG	CTG	GCACTTACCG	ATGCGAAGCC	ATCAACGCCA	GGGGATCAGC	1260
GTGGCTG	TCA	CGGTGGAATA	TGGTCCCCGG	AATTC		1295

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2214 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGAATCTTGA GTGGGATGCG GGACTCCCGT GCTATTTCTT GGC GGAGGTC TTTCTGGTC	60
CTTATGAGACA CCCCTGGTTT GGGATATGGG GGCGGCTAAG ATTTTCAGAGA TGGGGTCCCT	120
AGGCTGAGCC CGCGTTTTC CGGGCAGCGG TCGCGCTAGA ACCTTTCTGG GCGGACCTTC	180
AGCCCCGCGT GGCGCTCGTG GAGCGCGGGG GCTCGCTGTG GCTCAACTGC AGCACTAACT	240
GTCCGAGGCC GGAGCGCGGT GGYCTGGAGA CCTCGCTACG CCGAAACGGG ACCCAGAGGG	300
GTCTGCGCTG GCTGGCTCGA CAGMTGGTGG ACATCCGAGA GCCTGAAACC CAGTCGGTCT	360
GCTTCTTCGG CTGGGCGCGC CGCACACTCC AAGNAGTGG GCTCATCCGA ACTTTCAGC	420
GACCGGATCG GGTAGAGCTA GTGCCCTCGN CTCCTTGGCA GCCTGTAGGT GAGAACTTCA	480
CCTTAGAGTG CAGGGTCCCG GGGGCGAGAC CCCGAGCGAG CCTCACATG ACCTTGCTGC	540
GAGGCGGCCA GGAGCTGATT CGCCGAAGTT TCGTAGGCGA GCCACCCCGA GCTCGGGGTG	600
CGATGCTCAC CGCCACGGTC CTGGCGCGCA GAGAGGATCA CAGGGCCAAT TTCTCATGCC	660
TCGCGGAGCT TGACCTGCGG ACACACGGCT TGGGACTGTT TGCAACAGC TCAGCCCCCA	720
GACAGCTCCG CACGTTTGGC ATGCTCTCCAC TTTCCCCGAG CCTTATTGNC CCACGATTCT	780
TAGAAGTGGG CTCAGAAAGG CCGGTGACTT GCACCTTTGA TGGACTGTTT CCTGCCCCAG	840
AAGCCGGGT TTACCTCTCT CTGGGAGATC AGAGGCTTCA TCCTAATGTG ACCCTCGACG	900
GGGAGAGCCT TGTGGCCACT GNCACAGMTA CAGCAAGTGA AGAACAGGAA GGCACCAAAC	960
AGCTGATGTG CATCGTGACC CTCGGGGCGG AAGCAGGGA GACCCAGGAA AACCTGACTG	1020
TCTACAGCTT CCCGCTCCT CTTCTGACTT TAAGTGAGCC AGAAGCCCCC GAGGGAAAGA	1080
TGCTGACCGT AAGCTGTGCG GCAGGGGCCC GAGCCCTTGT CACCTTGGAG GGAATTCCAG	1140
CTGCGGTCCC TGGGCAGCCC GCTGAGCTCC AGTTAAATGT CACAAAGAAT GACGACAAAG	1200
GGGGCTTCTT CTGCGACGCT GCCCTCGATG TGGACGGGGA AACTCTGAGA AAGAACCAGA	1260
GCTCTGAGCT TCGTGTTCG TACGCACCTC GGCTGGATGA CTTGGACTGT CCCAGGAGCT	1320
GGACGTGGCC AGAGGGTCCA GAGCAGACCC TCCACTGCGA GGCCCGTGGA AACCCTGAGC	1380
CCTCCGTGCA CTGTGCAAGG CCTGACGGTG GGGCGGTGCT AGCGCTGGGC CTGTTGGGTC	1440
CAGTGACCCG TGCCCTCGCG GGAACCTTACC GATGTACAGC AATCAATGGG CAAGGCCAGG	1500
CGGTCAAGGA TGTGACCTTG ACTGTGGAAT ATGCCCCAGC GCTGGACAGT GTAGGCTGCC	1560
CAGAACGTAT TACTTGGCTG GAGGGGACAG AGGCATCGCT TAGCTGTGTG GCACACGGGG	1620
TCCCACCACC TAGCGTGAGC TGTGTGCGCT CTGGAAAGGA GGAAGTCATG GAAGGGCCCC	1680
TGCGTGTGGC CCGGGAGCAC GCTGGCACTT ACCGATGCGA AGCCATCAAC GNCAGGGGAT	1740
CAGCGGWC AAATGTGGCT GTCACGGTGG AATATGCTCC CAGTTTGGAG GAGTTGGGCT	1800

GCCCCAGYAA CTGGACTTGG GTAGAAGGAT CTGGAAGAACT GTTTTCCTGT GAAGTTGATG	1860
GGAAGCCGGA ACCACGCGTG GAGTGCCTGG GCTCGGAGGG TGCAAGCGAA GGGGTAGTGT	1920
TGCCCTCGGT GTCCTCGAAC TCTGGTTCCA GAAACTCTAT GACTCCTGGT AACCTGTCAC	1980
CGGGTATTTA CCTCTGCAAC GCCACCAACC GGMATGGNTC CACAGTCAAA ACAGTCGTCG	2040
TGAGCCCGGA ATCACCGCCA CAGATGGATG AATCCAGTTG CCCGAGTCAC CAGACATGGN	2100
TGGAAGGAGC CGAGGNTACT GCGCTGGCCT GCAGTGCCAG AGGNCGCCCC TCTCCACGCG	2160
TGCGCTGTTC CAGGGAAGGT GCAGMCAGGC TGGAGAGGNT ACAGGTGTCC CGAG	2214

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5077 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGAACGCTC CTCGCCCTCT GGTCTNCTCT GGNCTGGGG ATCCTAGGCA TCTCAGGTAA	60
GAAGAGCCCG CCCGTGGAGC NAGGTGGATA AGGCGGGGGC GGAATTGAAG GACCAGAGAG	120
GGCGGCCCGG GTGTCCCCTT CCAGGCTCCG CCCTCTTCTA GCTTCCCACG CTTCTGTCAC	180
CACCTGGAGN TCGGGGCTTC TCCCCTCTCT TCCTCCACCC CAACACACCT CAATCTTTCA	240
GANCTGAACC CAGCACCTTT TCTGGANING GGGNNITGCA CCTAACCTGT CTCAGGAGAN	300
ACTGTGGCTC TCCTGTCTCT TCCTGTCTCT TNA TGCCCTA TGGTTCACAG ACTGCGATCA	360
TCCTATATCA TGATCCTCAA AGACNCCATC TCCTCAACTG TCATAACTCA GAGCTCTATT	420
CCCCCTCCAC CTGGAGCCCT GGAAGCCGGC TTTCTAGGGC TTTTCTCCGC GGTTCCTTCC	480
CGGAGTTCAG CGTTGTGGCT TTTTGCCAA GTTACTCAAG TTGGGGGACA ATCTCCTTTA	540
AGCCTTTGAC TCAGTCTCAT TTCCACTTTG CTTTGGCCCC AAGCCTCTGT GTCTCTCCCC	600
CATTTCCTGA CGATCTGTCA GAGTCTTAAG AGTGATTGGG TTCCCATCC CCCCCTCCAA	660
TGGAGTCTCC TCCTCACTAT TGATGTGTGC ATCTGAGACC CCCATCCCCG CACCGAGTTT	720
CCCCATCTCT GTCACTAAGG AGCAAGGCTT CCAGAGACAA CCCTCTAATA GCGCGTCAGT	780
CCCGAATCTT GAGTGGGATG CGGGACTCCC GTGCTATTTC TTGGCGGAGG TCTTTCTCTG	840
TCCTTATGGA CACCCCTGGT TTGGGATATG GGGGCCGCTA AGATTTCAGA GATGGGGTCC	900
CTAGGCTGAG NCCGCGTTTT CCCGGGCAGC GGTGCGGCTA GAACCTTTCT GGGCGGACCT	960
TCAGCCCCGC GTGGCGCTCG TGGAGCGCGG GGGCTGCGTG TGGCTCAACT GCAGCACTAA	1020
CTGTCCGAGG CCGGAGCGCG GTGGCTGGA GACCTCGCTA CGCCGAAACG GGACCCAGAG	1080
GGTCTGNAC TGNTCTGGCT GACAGCTGGT GGACATCCGA GANCTGAAA CCCAGCCGGT	1140

CTGCTTCTTC	CNCTGCGCGC	GCCGCACACT	CCAAGCGCGT	GGGCTCATCC	GAACCTTCCG	1200
TGAGTTCAGG	GTGGGCACNC	CCCTTGGGTC	TCTGGACCTC	CCCCTCAAGC	TCCTCCACCC	1260
CGCCCTCTGA	TCCTCCTGCT	TGTTCTGAAA	GTACTACAGC	TGGCTAGAGC	GGAGTTTITG	1320
GTCCCTTGCA	GAGCGACCCG	ATCGGGTAGA	GCTAGTGCTT	CTGCCTCCTT	GGCAGCCTGT	1380
AGGTGAGAAC	TTACCTTTGA	GCTGCAGGGT	CCCGGGGGCA	GGACCCCGAG	CGAGCCTCAC	1440
ATTGACCTTG	CTGCGAGGGC	GCCAGGAGCT	GATTGCGCGA	AGTTTCGTAG	GCGAGCCACC	1500
CCGAGCTCGG	GGTGCAGTGC	TCACCGCCAC	GGTCTGGCG	GCGAGAGAGG	ATCACAGGGC	1560
CAATTTCTCA	TGCTTCGCGG	AGCTTGACCT	GCGNCCACAC	GGCTTGGGAC	TGTTTGCANA	1620
CAGCTCAGCC	CCCAGACAGC	TCCGCACTGT	TGGTGAGTGT	GGACCTTAAC	TGACAGATTT	1680
TAAGAAGTTT	AGGGCAGCCA	GGCGTGGTGG	CATGGTGTCG	TAGGCCCTAA	GTCCACGGCC	1740
AAGCAGANCT	AAGNCGGATC	TCITTGTGAAT	TAAAAGTCTA	GCTCGTCTAC	ATAACGAGGN	1800
CTGCATAGTT	AAATCCCCCA	AAAGCTAAG	CAGCTAGCCC	TTACTTCCAA	CACAAGTACT	1860
AGCTTAAAGTA	CTTTCTCCTG	TGAGCTTTTT	CCTTTATGTA	TTTACTCGTT	GAGAGAAAAA	1920
GAGAGTGTGT	GTACGTGCCT	TTATGCACAT	GCCGCAGTGC	TTGTATGGAA	GTTAAGAAGT	1980
AAGGAGGCGT	TCTGCCCTTC	CATCCTGTGG	GTCTTAGGGG	TGGTATTAGC	TCCTCAGGCT	2040
TTGTTAGTNA	CAAGCGCCTA	GGCTTGGGGA	GCCATCTCGC	CCGCTCCTCT	GTATCTTTAG	2100
GGTGAAACCA	GACAATGCAT	GCAAATTGGT	TGATCAACAC	TGAATGTTTA	GTTCTGTAAT	2160
TCAAGCTCTG	TTCTTTGTCT	TCCTCAGCCA	TGCTTCCACT	TTCCCCCGAG	CCTTATTGCC	2220
CCACGATTCT	TAGAAGTGGG	CTCAGAAAAG	CCGGTGACKT	GCACCTTGGA	TGGACTGTIT	2280
CCTGCCCCAG	AAGCCGGGGT	TTACTTCTCT	CTGGGAGATC	AGAGGCTTCA	TCCTAATGTG	2340
ACCCTCGAGC	GGGAGAGCCT	TGTGGCCACT	GCCACAGCTA	CAGCAAGTGA	AGAACAGGAA	2400
GGCACCAAAC	AGCTGATGTG	CATCGTGACC	CTCGGGGGCG	AAAGCAGGGA	GACCCAGGAA	2460
AACCTGACTG	TCTACAGTAA	GGGGAATCCA	ACAAGACCTT	CAATAGCTCA	GACTGGGGCT	2520
GGGGCTGGGT	CTGGGTCTGG	GGCCAGAGTC	TCACAAAGGC	GGAGCCTATA	AAGTGGGCGG	2580
GACCTCCACA	CCAGAACAAG	CCGGCGGGGA	GAGTTCACAG	GCGAGAGCAG	ATAGAAGTTG	2640
GAAATTAATA	GATTGGGTTG	AGTTCCCTGA	GTGGGGAGTG	AACCCCAACC	AATTCTCTGT	2700
CCCCAGGCTT	CCCGGCTCCT	CTTCTGACTT	TAAGTGAGCC	AGAAGCCCCC	GAGGGAAAGA	2760
TGCTGACCGT	AAGCTGTCTG	GCAGGGGCCC	GAGCCCTTGT	CACCTTGGAG	GGAATTCCAG	2820
CTCGGCTCCC	TGGGCAGCCC	GCTGAGCTCC	AGTTAAATGT	CACAAAGAAT	GACGACAAGC	2880
GGGGCTTCTT	CTGCGAGCCT	GCCCTCGATG	TGGACGGGGA	AACCTCTGGA	AGAACCAGA	2940
GCTCTGAGCT	TGCTGTTCTG	TGTGAGTGGA	TGTTCACTTT	ATCTCTGTGA	ATTCCAAGGA	3000
CCCTCTTACC	GGCCCCATCT	TTAACCTTAT	CGTATCCCTT	CTGCCTCATG	CCCGCAGAGC	3060

CACCTCGGCT	GGATGACTTG	GACTGTCCCA	GGAGCTGGAC	GTGGCCAGAG	GGTCCAGAGC	3120
AGACCCTCCA	CTGCGAGGCC	CSTGGAAACC	CTGAGCCCTC	CGTGCACTGT	GCAAGSCCTG	3180
ACGGTGGGGC	GGTGCTAGCG	CTGGGCTGT	TGGGTCCAGT	GACCCGTGCC	CTCGGGGCA	3240
CTTACCGATG	TACAGCAATC	AATGGGCAAG	GCCAGGCGGT	CAAGGATGTG	ACCTGTACTG	3300
TGGAATGTGA	TAGGGGGAG	GTGGGCATGC	TTATCCCTTT	AAGGTCACGG	AGTGTACTGG	3360
GAGACTGGCT	ATACGGAAAG	GAAAGAAGCC	TAGGTTGAGC	AGGGATTGGG	AAAACACTGA	3420
AGGAAAGTGG	TGTGTTGTTT	ACAAACTTAA	CGGTGGTAAC	TGGGCACGGT	CTGGCAAAAA	3480
CAGACAGCCA	AGAGAGTGTG	CCTGGGAAGC	TGCAATGGGG	GCTTTGTGGG	AATTGGTCAA	3540
CAGCACCCCTG	AGATCTCAGG	AAAGGGGCCT	GAAGTTATCT	CCAGAACCCA	TGTGAAGGCA	3600
GGAAGAGAGA	ACGCCCACTT	TTTCTGCTC	CCCCCAACCC	CCCCCACAT	ATCACACGGA	3660
GTATATAAAT	AAATAAAATG	GCTCCTGCCG	GAGGGAGTGA	GAAGCTGTCT	CCTGCAGGCT	3720
CAGAGCAGTG	GTAGTGATGC	CCTTTAATCC	CAGCACTCGG	TAGGCAAAGG	CAGGCAGATC	3780
TCGTGTAATG	TGGGGCCAGC	CTGGTCTGTA	CAGAGAAATC	CTGTCTCAAA	ACAAACCAGC	3840
AAAGAAACAA	AACCAAAATC	AATTCCAGAT	GCCCCAGCGC	TGGACAGTGT	AGGCTGCCCA	3900
NGACGTATTA	CTTGNTGGA	GGGGACAGAG	GCATCGCTTA	GCTGTGTGGC	ACACGGGGTC	3960
CCACCACCTA	GCCTGAGCTG	TGTGCGCTCT	GGAAAGGAGG	AAGTCATGGA	AGGGCCCTCG	4020
CGTGTGGCCC	GGGAGCACGC	TGGCACTTAC	CGATGCGAAG	CCATCAACGC	CAGGGGATCA	4080
GCGGNCAAAA	ATGTGGCTGT	CACGGTGGAA	TGTGAGTAGG	GGTGGCTACG	GAAATGTCCA	4140
CACCTGCGCT	CTCTGTCTCT	AGTGTGAACT	CCTATTTCCT	TGCTTCCTAG	ATGGTCCCAG	4200
TTNTGAGGAG	TTGGGCTGCC	CCAGCAACTG	GACTTGGGTA	GAAGGATCTG	GAAACTGTT	4260
TTCTGTGTA	GTGATGGGA	AGCCGGAACC	ACGCGTGGAG	TGCGTGGGCT	CGGAGGGTGC	4320
AAGCGAAGGG	GTAGTGTGTC	CCCTGGTGTG	CTCGAACTCT	GGTTCAGAA	ACTCTATGAC	4380
TCCTGGTAAC	CTGTACCCGG	GTATTACCT	CTGCAACGCG	ACCAACCGGC	ATGGCTCCAC	4440
AGTCAAAACA	GTCTGCTGA	GCGCGGAATG	TGAGCAGGGG	CCCAGGTGGG	CGGAGAGTAC	4500
CGGGTGTCCC	AGGATCTTTT	CTTTCCCTGA	TGCCCCCTCT	TATGGTGGCT	GATCTGCAGC	4560
ACCGCCACAG	ATGGATGAAT	CCAGTTGCCC	GAGTCACCAG	ACATGGCTGG	AAGGAGCCGA	4620
GGCTACTGCG	CTGGCCTGCA	GTGACAGGGG	NCGCCCTCT	CCACGCGTGC	GCTGTTCCAG	4680
GGAAGGTGCA	GCCAGGCTGG	AGAGGCTACA	GGTGTCCCAG	GAGGATGCGG	GGACCTACCT	4740
GTGTGTGGCT	ACCAACGCGC	ATGGCACGGA	TTACGCGACC	GTCACTGTGG	GTGTGGAATG	4800
TGAGTGAGGA	CAGCGCTGAA	TGAAGACGAC	TCAGACCGCC	AGAAAAGTGC	CTTGAGGCTT	4860
GGGATGTATG	ATCCAGTGGG	TAGAGTGTCT	AATTAGCACT	CACTAAAATG	TATATTCTAT	4920
TCCTAATACT	CTTTAATTTT	ANCTTTTGGG	AGGCAGAGAC	AGGCAGATCT	CTGTTCGGGG	4980

ATAACCTGCT CTCTGTCTAG GACAGCTTGG TCTACAGAGG GGNATACAGGC CCCCCCTCCC 5040
AAGATTGNAT AGCAACCCCTC TGGCTCCCTG TCTCTCT 5077

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1472 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

NGAATTCGCG	CGGATCGGGT	AGAGCTAGTG	CCTCTGCCTC	CTTGGCAGCC	TGTAGTGAG	60
AACTTCACCT	TGAGCTGCAG	GGTCCCGGGG	GCAGGACCCC	GAGCGAGCCT	CACATTGACC	120
TTGCTGCGAG	GCGGCCAGGA	GCTGATTGCG	CGAAGTTTCG	TAGGCGAGCC	ACCCCGAGCT	180
CGGGGTGCGA	TGCTCACC GC	CACGGTCCTG	GCGCGCAGAG	AGGATCACAG	GGCCAATTTC	240
TCATGCTCTG	CGGAGCTTGA	CCTGCGGCCA	CACGGCTTGG	GACTGTTTGC	AAACAGCTCA	300
GCCCCCAGAC	AGCTCCGCAC	GTTTGCCATG	CCTCCACTTT	CCCCGAGCCT	TATTGCCCCA	360
CGATTCTTAG	AAGTGGGCTC	AGAAAGGCCG	GTGACTTGCA	CTTTGGATGG	ACTGTTTCCT	420
GCCCCCAGA	CGGGGGTTTA	CCTCTCTCTG	GGAGATCAGA	GGCTTCATCC	TAATGTGACC	480
CTCGACGGGG	AGAGCCTTGT	GGCCACTGCC	ACAGCTACAG	CAAGTGAAGA	ACAGGAAGGC	540
ACCAAACAGC	TGATGTGCAT	CGTGACCCTC	GGGGCGGAAA	GCAGGGAGAG	CCAGGAAAAC	600
CTGACTGTCT	ACAGCTTCCC	GGCTCCTCTT	CTGACTTTAA	GTGAGCCAGA	AGCCCCGAG	660
GGAAAGATGG	TGACCGTAAG	CTGCTGGGCA	GGGGCCCGAG	CCCTTGTCAC	CTTGGAGGGA	720
ATTCCAGCTG	CGGTCCCTGG	GCAGCCCGCT	GAGCTCCAGT	TAAATGTCAC	AAAGAATGAC	780
GACAAGCGGG	GCTTCTTCTG	CGACGCTGCC	CTCGATGTGG	ACGGGGGAAA	TCTGAGAAAG	840
AACCAGAGCT	CTGAGCTTCG	TGTTCTGTGT	GAGTGGATGT	TCACTTTATC	TCTGTGAATT	900
CCAAGGACCC	TCTTACCGGC	CCCATCTTTA	ACCTTATCGT	ATCCCCCTCT	CCTCATGCCC	960
GCAGACGCAC	CTCGGCTGGA	TGACTTGGAC	TGTCCCAGGA	GCTGGACGTG	GCCAGAGGGT	1020
CCAGAGCAGA	CCCTCCAATG	CGAGGCCCGT	GGAAACCCCT	AGCCCTCCGT	GCACTGTGCA	1080
AGGCCTGACG	GTGGGGCGGT	GCTAGCGCTG	GGCCTGTTGG	GTCCAGTGAC	CCGTGCCCTC	1140
GCGGGCACTT	ACCGATGTAC	AGCAATCAAT	GGGCAAGGCC	AGGCGGTCAA	GGATGTGACC	1200
CTGACTGTGG	AATATGCCCC	AGCGCTGGAC	AGTGTAGGCT	GCCCAGAACG	TATTACTTGG	1260
CTGGAGGGGA	CAGAGGCATC	GCTTAGCTGT	GTGGCACACG	GGGTCCCACC	ACCTAGCGTG	1320
AGCTGTGTGC	GCTCTGGAAA	GGAGGAAGTC	ATGGAAGGGC	CCCTGCGTTT	TGCGCCGGAG	1380
CACGCTGGCA	CTTACCGATG	CGAAGCCATC	AACGCCAGGG	GATCAGCGGC	CAAAAATGTG	1440

GCTGTCACGG TGGAATATGG TCCCCGGAAT TC

1472

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2550 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCTCTGCCTC	CTTGGCAGCC	TGTAGGTGAG	AACTTCACCT	TGAGCTGCAG	GGTCCCGGGG	60
GCAGGACCCC	GAGCGAGCCT	CACATTGACC	TTGCTGCGAG	GCGGCCAGGA	GCTGATTTCG	120
CGAAGTTTCG	TAGGCGAGCC	ACCCCGAGCT	CGGGGTGCGA	TGCTCACCGC	CACGGTCTCTG	180
GCGGCGAGAG	AGGATCACAG	GGCCAATTTC	TCATGCCTCG	CGGAGCTTGA	CCTGCGGCCA	240
CACGGCTTGG	GACTGTTTGC	AAACAGCTCA	GCCCCAGAC	AGCTCCGCAC	GTTTGCCATG	300
CCTCCACTTT	CCCCGAGCCT	TATTGCCCCA	CGATTCTTAG	AAGTGGGCTC	AGAAAGGCCG	360
GTGACTTGCA	CTTTGGATGG	ACTGTTTCCT	GCCCCAGAAG	CGGGGGTTTA	CCTCTCTCTG	420
GGAGATCAGA	GGCTTCATCC	TAATGTGACC	CTCGACGGGG	AGAGCCTTGT	GGCCACTGCC	480
ACAGTACAG	CAAGTGAAGA	ACAGGAAGGC	ACCAAACAGC	TGATGTGCAT	CGTGACCCTC	540
GGGGCGGAAA	GCAGGGAGAC	CCAGGAAAAA	CTGACTGTCT	ACAGCTTCCC	GGCTCCTCTT	600
CTGACTTTAA	GTGAGCCAGA	AGCCCCCGAG	GGAAAGATGG	TGACCGTAAG	CTGCTGGGCA	660
GGGGCCCGAG	CCCTTGTTCAC	CTTGGAGGGA	ATTCCAGCTG	CGGTCCCTGG	GCAGCCCGCT	720
GAGCTCCAGT	TAAATGTCAC	AAAGAATGAC	GACAAGCGGG	GCTTCTTCTG	CGACGCTGCC	780
CTCGATGTGG	ACGGGGAAAC	TCTGAGAAAG	AACCAGAGCT	CTGAGCTTCG	TGTTCTGTAC	840
GCACCTCGGC	TGGATGACTT	GGACTGTCCC	AGGAGCTGGA	CGTGCCGAGA	GGGTCCAGAG	900
CAGACCCCTC	ACTGCGAGGC	CCGTGGA AAC	CCTGAGCCCT	CCGTGCACTG	TGCAAGGCCT	960
GACGGTGGGG	CGGTGCTAGC	GCTGGGCCCT	TTGGGTCCAG	TGACCCGTGC	CCTCGCGGGC	1020
ACTTACC GAT	GTACAGCAAT	CAATGGGCAA	GGCCAGGCGG	TCAAGGATGT	GACCTGACT	1080
GTGGAATATG	CCCCAGCGCT	GGACAGTGTA	GGCTGCCCAG	AACGTATTAC	TTGGCTGGAG	1140
GGGACAGAGG	CATCGCTTAG	CTGTGTGGCA	CACGGGGTCC	CACCACCTAG	CGTGAGCTGT	1200
GTGCGCTCTG	GAAAGGAGGA	AGTCATGGAA	GGGCCCTTGC	GTGTGGCCCC	GGAGCACGCT	1260
GGCACTTACC	GATGCGAAGC	CATCAACGCC	AGGGGATCAG	CGGCCAAAAA	TGTGGCTGTC	1320
ACGGTGGAAT	ATGTGCCCAG	TTTTGAGGAG	TTGGGCTGCC	CCAGCAACTG	GACTTGGGTA	1380
GAAGGATCTG	GA AA ACTGTT	TTCTGTGAA	GTTGATGGGA	AGCCGGAACC	ACGCGTGGAG	1440
TGCGTGGGCT	CGGAGGGTGC	AAGCGAAGGG	GTAGTGTGTC	CCCTGGTGTC	CTCGAACTCT	1500

GGITCCAGAA ACTCTATGAC TCCTGGTAAC CTGTCACCGG GTATTTACCT CTGCAACGCC	1560
ACCAACCGGC ATGGGCTCCAC AGTCAAACA GTCGTCGTGA GCGCGGAATC ACGGCCACAG	1620
ATGGATGAAT CCAGTTGCCC GAGTACCAG ACATGGCTGG AAGGAGCCGA GGCTACTGCG	1680
CTGGCCTGCA GTGCCAGAG CCGCCCTCT CCACGCGTGC GCTGTTCCAG GGAAGGTGCA	1740
GCCAGGCTGG AGAGGCTACA GGTGTCCGA GAGGATGCGG GGACCTACCT GTGTGTGGCT	1800
ACCAACGCGC ATGGCACGGA TTCACGACC GTCACCTGCG GTGTGGAATA CCGGCCTGTG	1860
GTGGCTGAGC TGGCAGCCTC GCCCCCAAGC GTGCGGCCTG GCGGAACTT CACTCTGACC	1920
TGCCGTGCAG AGGCCTGGCC TCCAGCCAG ATCAGCTGGC GCGCGCCCC GGGAGCTCTC	1980
AACCTCGGTC TCTCCAGCA CAACAGCAGC CTGAGCGTGG CCGGTGCCAT GGGCAGCCAT	2040
GTGGCGGAGT ATGAGTGCGC AGCCACCAAT GCGCATGGGC GCCACGCAGC GCGCATCAGC	2100
GTGCGCGTGG COGGTCCATG GCTGTGGGTC GCTGTGGGCG GTGCGGCAGG GGGCGCGGCG	2160
CTGCTGGCCG CAGGGGCGCG CCTGGCCTTC TACGTGCAGT CCACCGCTTG CAAGAAGGGA	2220
GAGTACAACG TCCAGGAGGC TGAGAGCTCA GCGCAGGCGG TGTGTCTCAA TGGCGCGGGC	2280
GGGACACCGG GTGCAGAAGG CGGAGCAGAG ACCCCCGGCA CTGCCGAGTC ACCTGCAGAT	2340
GGCGAGGTTT TCGCCATCCA GCTGACATCT TCCTGAGCCT GTATCCAGCT CCCCAGGGG	2400
CCTCGAAAGC ACAGGGGTGG ACGTATGTAT TGTCTACTCT CTATTATTTC AACTCCAGGG	2460
GCGTCGTCCC CGTTTTCTAC CCATTCCCTT AATAAAGTTT TTATAGGAGA AAAAAAAAAA	2520
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2550

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AATTCGATCA CTGCGCTCC CCTCGCCTTC TCGCTCTCC CCTCCCTGGC AGCGGCGGCA	60
ATGCCGGGGC CTTCACCAGG GCTGCGCGCA ACGCTCCTCG GCCTCTGGGC TGCCCTGGGC	120
CTGGGATCC TAGGCATCTC AGCGGTGCGC CTAGAACCTT TCTGGGCGGA CCTTCAGCCC	180
C GCGTGGCGC TCGTGGAGCG CGGGGCTCG CTGTGGCTCA AC	222

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGTGGAGCTG GCACCCCTGC CTCCTTGGCA GCCGGTGGGC CAGAACTTCA CCCTGCGCTG	60
CCAAGTGGAG GGTGGGTGCG CCCGGACCAG CCTCACGGTG GTGCTGCTTC GCTGGGAGGA	120
GGAGCTGAGC CGGCAGCCCG CAGTGGAGGA GCCAGCGGAG GTCACTGCCA CTGTGCTGGC	180
CAGCAGAGAC GACCACGGAG CCCCTTTCTC ATGCCGCACA GAACTGGACA TGCAGCCCCA	240
GGGGCTGGGA CTGTTCTGTA ACACCTCAGC CCCCCGCCAG CTCGGAACCT TT	292

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro	Asp	Arg	Val	Glu	Leu	Val	Pro	Leu	Pro	Pro	Trp	Gln	Pro	Val	Gly
1					5				10					15	
Glu	Asn	Phe	Thr	Leu	Ser	Cys	Arg	Val	Pro	Gly	Ala	Gly	Pro	Arg	Ala
			20					25					30		
Ser	Leu	Thr	Leu	Thr	Leu	Leu	Arg	Gly	Gly	Gln	Glu	Leu	Ile	Arg	Arg
			35				40					45			
Ser	Phe	Val	Gly	Glu	Pro	Pro	Arg	Ala	Arg	Cys	Ala	Met	Leu	Thr	Ala
			50				55				60				
Thr	Val	Leu	Ala	Arg	Arg	Glu	Asp	His	Arg	Asp	Asn	Phe	Ser	Cys	Leu
			65		70				75					80	
Ala	Glu	Leu	Asp	Leu	Arg	Thr	His	Gly	Leu	Gly	Leu	Phe	Ala	Asn	Ser
			85					90						95	
Ser	Ala	Pro	Arg	Gln	Leu	Arg	Thr	Phe							
			100				105								

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAACCTGAGG CCATGCCTCC ACTTTCC

27

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCATAAGCTT TATTCCACCG TGACAGCCAC

30

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AACGTGCGGA GCTGTCTG

18

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACGGAATTGC AAGCCATCAA CCCCAGG

27

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CATGAATTCC GAATCTTGAG TGGGATG

27

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
ATAGAATTCC TCGGGACACC TGTAGCC 27
- (2) INFORMATION FOR SEQ ID NO:20:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
CARGGTGACA AGGGCTCG 18
- (2) INFORMATION FOR SEQ ID NO:21:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
TATGAATTCA GTTGAGCCAC AGCGAGC 27
- (2) INFORMATION FOR SEQ ID NO:22:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
CCGGGTCTTA GAGGTGGACA CGCA 24
- (2) INFORMATION FOR SEQ ID NO:23:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
TGCACTGTCT CTTGCTCTG GTTC 24
- (2) INFORMATION FOR SEQ ID NO:24:
- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 992 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCGAAAACCG GGAGACCCGG GAGAACGTGA CCATCTACAG CTTCCTCCGGCA CCACTCCTGA	60
CCCTGAGCGA ACCCAGCGTC TCCGAGGGGC AGATGGTGAC AGTAACCTGC GCAGCTGGGG	120
CCCAAGCTCT GTTCACACTG GAGGGAGTTC CAGCCGCGGT CCCGGGGCAG CCCGCCAGC	180
TTCAGCTAAA TGCCACCGAG AACGACGACA GACGCAGCTT CTTCGTGCGC GCCACCTCG	240
ATGTGGACGG GGAGACCCCTG ATCAAGAACA GGAGCGCAGA GCTTCGTGTC CTATACGCTC	300
CCGGCTAGA CGATTCGGAC TGCCCCAGGA GTTGGACGTG GCCCGAGGGC CCAGAGCAGA	360
CGCTGCGCTG CGAGGCCCGC GGGAAACCCAG AACCTCAGT GCACTGTGCG CGTCCGACG	420
GCGGGGCCGT GCTGGCTCTG GGCCTGCTGG GTCCAGTCAC TCGGGCGCTC TCAGGCACTT	480
ACCGCTGCAA GCGCGCCAAT GATCAAGGCG AGGCGGTCAA GGACGTAACG CTAACGGTGG	540
AGTACGCACC AGCGTGGAC AGCGTGGGCT GCCCAGAACG CATTACTTGG CTGGAGGGAA	600
CAGAAGCCTC GCTGAGCTGT GTGGCGCACG GGGTACCGCC GCCTGATGTG ATCTGCGTGC	660
GCTCTGGAGA ACTCGGGGCC GTCACTGAGG GGCTGTGCG TGTGGCCCGG GAGCATGCGG	720
GCACTTACCG CTGCGAAGCC ACCAACCTC GGGGCTCTGC GGCCAAAAAT GTGGCCGTCA	780
CGGTGGAATA TGGCCCCAGG TTTGAGGAGC CGAGCTGCCC CAGCAATTGG ACATGGGTGG	840
AAGGATCTGG GCGCCTGTTT TCCTGTGAGG TCGATGGGAA GCCACAGCCA AGCGTGAAGT	900
GCGTGGGCTC CGGGGGCACC ACTGAGGGGG TGCTGTGCTC GCTGGCACCC CCAGACCCTA	960
GTCCAGAGC TCCAGAAATC CCTAGAGTCC TG	992

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2775 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCAGCCTCGC GTGGCGTTCTG TGGAGCGCGG GGGCTCGCTG TGCTGAATT GCAGCACCAA	60
CTGCCCTCGG CCGGAGCGCG GTGGCCTGGA GACCTCGCTG CGCCGAAACG GGACCCAGAG	120
GGGTTTGCGT TGGTTGCGC GGCAGCTGGT GGACATTGCG GAGCCGAGAGA CTCAGCCCGT	180
CTGCTTCTTC CGCTGCGCGC GGCACACT ACAGGCGCGT GGGCTCATTC GCACTTTCCA	240

GCGACCAGAT	CGCGTAGAGC	TGATGCCGCT	GCCTCCCTGG	CAGCCGGTGG	GCGAGAACTT	300
CACCTGAGC	TGTAGGTTCC	CCGGCGCCGG	GCCCCGTGCG	AGCCTCACGC	TGACCCTGCT	360
GCGGGGCGCC	CAGGAGCTGA	TCCGCCGCG	CTTCGCCGGT	GAACCACCCC	GAGCGCGGGG	420
GCGGGTGTCT	ACAGCCACGG	TACTGGCTCG	GAGGAGGAC	CATGGAGCCA	ATTTCCTGCTG	480
TCCGCCCGAG	CTGGACCTGC	GGCCGCACGG	ACTGGGACTG	TTTGAAAACA	GCTCGGCCCC	540
CAGAGAGCTC	CGAACCTTCT	CCCTGTCTCC	GGATGCCCGG	CGCCTCGCTG	CTCCCCGCT	600
CTTGGAAGTT	GGCTCGGAAA	GGCCCGTGAG	CTGCACTCTG	GACGGACTGT	TTCAGCCTC	660
AGAGGCCAGG	GTCTACCTCG	CACTGGGGGA	CCAGAATCTG	AGTCCTGATG	TCACCCTCGA	720
AGGGGACGCA	TTCTGGGCCA	CTGCCACAGC	CACAGCTAGC	GCAGAGCAGG	AGGGTGCCAG	780
GCAGCTGGTC	TGCAACGTCA	CCCTGGGGGG	CGAAAACCGG	GAGACCCGGG	AGAACGTGAC	840
CATCTACAGC	TTCCCGGCAC	CACCTCTGAC	CCTGAGCGAA	CCCAGCGTCT	CCGAGGGGCA	900
GATGGTGACA	GTAACCTGCG	CAGCTGGGGC	CCAAGCTCTG	GTCACTCTGG	AGGGAGTTCC	960
AGCCGCGGCT	CCGGGGCAGC	CCGCCAGCT	TCAGCTAAAT	GCCACCGAGA	ACGACGACAG	1020
ACGCAGCTTC	TTCTGCGACG	CCACCCTCGA	TGTGGACGGG	GAGACCTTGA	TCAAGAACAG	1080
GAGCGCAGAG	CTTCGTGTCC	TATACGCTCC	CCGGCTAGAC	GATTCGGACT	GCCCCAGGAG	1140
TTGGACGTGG	CCCGAGGGCC	CAGAGCAGAC	GCTGCGCTGC	GAGGCCCGCG	GGAACCCAGA	1200
ACCCCTCAGT	CAGTGTGCGC	GCTCCGACGG	CGGGGCCGTG	CTGGCTCTGG	GCCTGCTGGG	1260
TCCAGTCACT	CGGGCGCTCT	CAGGCACCTA	CCGCTGCAAG	GCGGCCAATG	ATCAAGGCGA	1320
GGCGGTCAAG	GACGTAACGC	TAACGGTGA	GTACGCACCA	GCGCTGAGCA	GCGTGGGCTG	1380
CCCAGAAGCG	ATTACTTGGC	TGGAGGGAAC	AGAAGCCTCG	CTGAGCTGTG	TGGCGCACGG	1440
GGTACCGCCG	CCTGATGTGA	TCTGCGTGCG	CTCTGGAGAA	CTCGGGGCCG	TCATCGAGGG	1500
GCTGTTGCGT	GTGGCCCGGG	AGCATGCGGG	CACCTTACCGC	TGCGAAGCCA	CCAACCCTCG	1560
GGGCTCTCGG	GCCAAAATG	TGGCCGTCAC	GGTGGAATAT	GGCCCAGGT	TTGAGGAGCC	1620
GAGCTGCCCC	AGCAATTGGA	CATGGGTGGA	AGGATCTGGG	CGCCTGTTTT	CCTGTGAGGT	1680
CGATGGGAAG	CCACAGCCAA	CGGTGAAGTG	CGTGGGCTCC	GGGGGCACCA	CTGAGGGGGT	1740
GCTGCTGCCG	CTGGCACCCC	CAGACCCTAG	TCCCAGAGCT	CCCAGAATCC	CTAGAGTCTT	1800
GGCACCCGGT	ATCTACGTCT	GCAACGCCAC	CAACCGCCAC	GGCTCCGTGG	CCAAAACAGT	1860
CGTCGTGAGC	GCGGAGTCGC	CACCGGAGAT	GGATGAATCT	ACCTGCCCAA	GTCACCAGAC	1920
GTGGCTGGAA	GGGGCTGAGG	CTTCCGCGCT	GGCCTGCGCC	GCCCCGGGTC	GGCCTTCCCC	1980
AGGAGTGCGC	TGCTCTCGGG	AAGGCATCCC	ATGGCTGTAG	CAGCAGCGCG	TGTCCTCGAGA	2040
GGACGCGGGC	ACTTACCACT	GTGTGGCCAC	CAATGCGCAT	GGCACGGACT	CCCCGACCGT	2100
CACTGTGGGC	GTGGAATACC	GGCCAGTGGT	GGCCGAACCT	GCTGCCTCGC	CCCCTGGAGG	2160

CGTGCGCCCA GGAGGAAACT TCACGTTGAC CTGCCGCGCG GAGGCCCTGGC CTCCAGCCCA	2220
GATCAGCTGG CGCGCGCCCC CGAGGGCCCT CAACATCGGC CTGTCGAGCA ACAACAGCAC	2280
ACTGAGCGTG GCAGGCGCCA TGGGAAGCCA CGGCGGCGAG TACGAGTGGC CACGCACCAA	2340
CGCGCACGGG CGCCACGCGC GCGGCATCAC GGTGCGCGTG GCCGCTCCGT GGCTATGGGT	2400
CGCCGTGGGC GGC GCGCGCGG GGGGCGCGGC GCTGCTGGCC GCGGGGGCCG GCCTGGCCTT	2460
CTACGTGCAG TCCACCGCCT GCAAGAAGGG CGAGTACAAC GTGCAGGAGG CCGAGAGCTC	2520
AGGCGAGGCT GTGTGCTGA ACGGAGCGGG CGGCGGCGCT GCGGGGGCGG CAGGCGCGGA	2580
GGGCGGACCC GAGGCGGCGG GGGGCGCGGC CGAGTCGCCG GCGGAGGGCG AGGTCTTCGC	2640
CATACAGCTG ACATCGGCGT GAGCCCGCTC CCTCTCCGC GGGCCGGGAC GCCCCCCAGA	2700
CTCACACGGG GGCTTATTIA TTGCTTTATT TATTACTTA TTCATTTATT TATGTATTCA	2760
ACTCCAAGGG AATTCT	2775

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1557 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CGCGCTCTCT TCGCCTCCTG TGCTTTCCCC GCGCGGCGGA TGCCAGGGCC TTCGCCAGGG	60
CTGCGCGCGG CGTACTCGG CCTCTGGGCT GCTCTGGGCC TGGGGCTCTT CGGCTCTCA	120
GCGTCTCGC AGGAGCCCTT CTGGGCGGAC CTGCAGCTC GCGTGGCGTT CGTGGAGCGC	180
GGGGGCTCGC TGTGGCTGAA TTGCAGCACC AACTGCCCTC GGGCGGAGCG CGTGGCCCTG	240
GAGACCTCGC TGCGCCGAAA CGGGACCCAG AGGGGTTTGC GTTGGTTGGC GCGGCAGCTG	300
GTGGACATTC GCGAGCCGGA GACTCAGCCC GTCTGCTTCT TCCGCTCGGC GCGCGGCACA	360
CTACAGGCGC GTGGGCTCAT TCGCACTTTC CAGCGACCAG ATCGCGTAGA GCTGATGCCG	420
CTGCCTCCCT GGCAGCCGGT GGGCGAGAAC TTCACCTGA GCTGTAGGGT CCCGCGGCC	480
GGGCCCCGTG CGAGCCTCAC GCTGACCCTG CTGCGGGGCG CCCAGGAGCT GATCCGCCGC	540
AGCTTCGCCG GTGAACCACC CCGAGCGCGG GCGCGGGTGC TCACAGCCAC GGTACTGGCT	600
CGGAGGGAGG ACCATGGAGC CAATTTCTCG TGTGCGGCCG AGCTGGACCT GCGGCCGCAC	660
GGACTGGGAC TGTTTGAAAA CAGCTCGGCC CCCAGAGAGC TCCGAACCTT CTCCTGTCT	720
CCGSATGCCC CGCGCCTCGC TGCTCCCGCG CTCTTGGAAG TTGGCTCGGA AAGGCCCGTG	780
AGCTGCACCT TGGACGGACT GTTTCAGGCC TCAGAGGCCA GGGTCTACCT CGCACTGGGG	840
GACCAGAATC TGAGTCTCTG TGTCAACCTC GAAGGGGACG CATTCTGTGC CACTGCCACA	900

GCCACAGCTA GCGCAGAGCA GGAGGGTGCC AGGCAGCTGG TCTGCAACGT CACCCCTGGG	960
GGCGAAAACC GGGAGACCCG GGAGAACGTG ACCATCTACA GCTTCCCAGC ACCACTCCTG	1020
ACCCCTGAGCG AACCCAGCGT CTCGAGGGG CAGATGGTGA CAGTAACCTG CGCAGCTGGG	1080
GCCCAAGCTC TGGTCACTT GGAGGGAGTT CCAGCCGCGG TCCCGGGCCA GCCCGCCAG	1140
CTTCAGCTAA ATGCCACCGA GAACGACGAC AGACGCGAGT TCTTCTGCGA CGCCACCCTC	1200
GATGTGGAGC GGGAGACCCG GATCAAGAAC AGGAGCGCAG AGCTTCGTGT CCTATACGCT	1260
CCCCGGCTAG ACGATTCCGA CTGCCCCAGG AGTTGGACGT GGCCCGAGGG CCCAGAGCAG	1320
ACGCTGCGCT GCGAGGCCCG CGGGAACCCA GAACCCCTCAG TGCAGCTGTC GCGCTCCGAC	1380
GGCGGGGCCG TGCTGGCTCT GGGCCTGCTG GGTCCAGTCA CTCGGGCGCT CTCAGGCAGT	1440
TACCGTGCAG AGGCGGCCAA TGATCAAGGC GAGGCGGTCA AGGACGTAAC GCTAACGGTG	1500
GAGTACGCAC CAGCGCTGGA CAGCGTGGGC TGCCCGAAGC GCATTACTTG GCTGGAG	1557

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2927 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 40..2814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CGCGCTCTCC TCGCCTCCTG TGCTTCCCC GCCGCGCG ATG CCA GGG CCT TCG	54
Met Pro Gly Pro Ser	
1 5	
CCA GGG CTG CGC CGG GCG CTA CTC GGC CTC TGG GCT GCT CTG GGC CTG	102
Pro Gly Leu Arg Arg Ala Leu Leu Gly Leu Trp Ala Ala Leu Gly Leu	
10 15 20	
GGG CTC TTC GGC CTC TCA GCG GTC TCG CAG GAG CCC TTC TGG GCG GAC	150
Gly Leu Phe Gly Leu Ser Ala Val Ser Gln Glu Pro Phe Trp Ala Asp	
25 30 35	
CTG CAG CCT CGC GTG GCG TTC GTG GAG CGC GGG GGC TCG CTG TGG CTG	198
Leu Gln Pro Arg Val Ala Phe Val Glu Arg Gly Ser Leu Trp Leu	
40 45 50	
AAT TGC AGC ACC AAC TGC CCT CGG CCG GAG CGC GGT GGC CTG GAG ACC	246
Asn Cys Ser Thr Asn Cys Pro Arg Pro Glu Arg Gly Gly Leu Glu Trp	
55 60 65	
TCG CTG CGC CGA AAC GGG ACC CAG AGG GGT TTG CGT TGG TTG GCG CGG	294
Ser Leu Arg Arg Asn Gly Thr Gln Arg Gly Leu Arg Trp Leu Ala Arg	
70 75 80 85	

CAG CTG GTG GAC ATT CGC GAG CCG GAG ACT CAG CCC GTC TGC TTC TTC Gln Leu Val Asp Ile Arg Glu Pro Glu Thr Gln Pro Val Cys Phe Phe	342
CGC TGC GCG CGG CGC ACA CTA CAG GCG CGT GGG CTC ATT CGC ACT TTC Arg Cys Ala Arg Arg Thr Leu Gln Ala Arg Gly Leu Ile Arg Thr Phe	390
CAG CGA CCA GAT CGC GTA GAG CTG ATG CCG CTG CCT CCC TGG CAG CCG Gln Arg Pro Asp Arg Val Glu Leu Met Pro Leu Pro Trp Gln Pro	438
GTG GGC GAG AAC TTC ACC CTG AGC TGT AGG GTC CCC GGC GCC GGG CCC Val Gly Glu Asn Phe Thr Leu Ser Cys Arg Val Pro Gly Ala Gly Pro	486
CGT GCG AGC CTC ACG CTG ACC CTG CTG CCG GGC GCC CAG GAG CTG ATC Arg Ala Ser Leu Thr Leu Thr Leu Leu Arg Gly Ala Gln Glu Leu Ile	534
CGC CGC AGC TTC GCC GGT GAA CCA CCC CGA GCG CGG GGC GCG GTG CTC Arg Arg Ser Phe Ala Gly Glu Pro Pro Arg Ala Arg Gly Ala Val Leu	582
ACA GCC ACG GTA CTG GCT CGG AGG GAG GAC CAT GGA GCC AAT TTC TCG Thr Ala Thr Val Leu Ala Arg Arg Glu Asp His Gly Ala Phe Ser	630
TGT CGC GCC GAG CTG GAC CTG CGG CCG CAC GGA CTG GGA CTG TTT GAA Cys Arg Ala Glu Leu Asp Leu Arg Pro His Gly Leu Leu Phe Glu	678
AAC AGC TCG GCC CCC AGA GAG CTC CGA ACC TTC TCC CTG TCT CCG GAT Asn Ser Ser Ala Pro Arg Glu Leu Arg Thr Phe Ser Leu Ser Pro Asp	726
GCC CCG CGC CTC GCT GCT CCC CGG CTC TTG GAA GTT GGC TCG GAA AGG Ala Pro Arg Leu Ala Ala Pro Arg Leu Leu Glu Val Gly Ser Glu Arg	774
CCC GTG AGC TGC ACT CTG GAC GGA CTG TTT CCA GCC TCA GAG GCC AGG Pro Val Ser Cys Thr Leu Asp Gly Leu Leu Pro Ala Ser Glu Ala Arg	822
GTC TAC CTC GCA CTG GGG GAC CAG AAT CTG AGT CCT GAT GTC ACC CTC Val Tyr Leu Ala Leu Gly Asp Gln Asn Leu Ser Pro Asp Val Thr Leu	870
GAA GGG GAC GCA TTC GTG GCC ACT GCC ACA GCC ACA GCT AGC GCA GAG Glu Gly Asp Ala Phe Val Ala Thr Ala Thr Ala Thr Ala Ser Ala Glu	918
CAG GAG GGT GCC AGG CAG CTG GTC TGC AAC GTC ACC CTG GGG GGC GAA Gln Glu Gly Ala Arg Gln Leu Val Cys Asn Val Thr Thr Gly Gly Glu	966
AAC CGG GAG ACC CGG GAG AAC GTG ACC ATC TAC AGC TTC CCG GCA CCA Asn Arg Glu Thr Arg Glu Asn Val Thr Ile Tyr Ser Phe Pro Ala Pro	1014
CTC CTG ACC CTG AGC GAA CCC AGC GTC TCC GAG GGG CAG ATG GTG ACA Leu Leu Thr Leu Ser Glu Pro Ser Val Ser Glu Gly Gln Met Val Thr	1062

GTA ACC TGC GCA GCT GGG GCC CAA GCT CTG GTC ACA CTG GAG GGA GTT Val Thr Cys Ala Ala Gly Ala Gln Ala Leu Val Thr Leu Gly Val	1110
345 350 355	
CCA GCC GCG GTC CCG GGG CAG CCC GCC CAG CTT CAG CTA AAT GCC ACC Pro Ala Ala Val Pro Gly Gln Pro Ala Gln Leu Gln Asn Ala Thr	1158
360 365 370	
GAG AAC GAC GAC AGA CGC AGC TTC TTC TGC GAC GCC ACC CTC GAT GTG Glu Asn Asp Asp Arg Arg Ser Phe Phe Cys Asp Thr Leu Asp Val	1206
375 380 385	
GAC GGG GAG ACC CTG ATC AAG AAC AGG AGC GCA GAG CTT CGT GTC CTA Asp Gly Glu Thr Leu Ile Lys Asn Arg Ser Ala Glu Leu Arg Val Leu	1254
390 395 400	
TAC GCT CCC CGG CTA GAC GAT TCG GAC TGC CCC AGG AGT TGG ACG TGG Tyr Ala Pro Arg Arg Asp Asp Ser Asp Cys Pro Arg Ser Trp Thr Trp	1302
410 415 420	
CCC GAG GGC CCA GAG CAG ACG CTG CGC TGC GAG GCC CGC GGG AAC CCA Pro Glu Gly Pro Glu Gln Thr Leu Arg Cys Glu Ala Arg Gly Asn Pro	1350
425 430 435	
GAA CCC TCA GTG CAC TGT GCG CGC TCC GAC GGC GGG GCC GTG CTG GCT Glu Pro Ser Val His Cys Ala Arg Ser Asp Gly Gly Ala Val Leu Ala	1398
440 445 450	
CTG GGC CTG CTG GGT CCA GTC ACT CGG GCG CTC TCA GGC ACT TAC CGC Leu Val Glu Leu Leu Gly Pro Val Thr Arg Ala Leu Ser Gly Thr Tyr Arg	1446
455 460 465	
TGC AAG GCG GCC AAT GAT CAA GGC GAG GCG GTC AAG GAC GTA ACG CTA Cys Lys Ala Ala Asn Asp Gln Gly Glu Ala Val Lys Asp Val Thr Leu	1494
470 475 480 485	
ACG GTG GAG TAC GCA CCA GCG CTG GAC AGC GTG GGC TGC CCA GAA CGC Thr Val Glu Tyr Ala Pro Ala Leu Asp Ser Val Gly Cys Pro Glu Arg	1542
490 495 500	
ATT ACT TGG CTG GAG GGA ACA GAA GCC TCG CTG AGC TGT GTG GCG CAC Ile Thr Trp Leu Glu Gly Thr Glu Ala Ser Leu Ser Cys Val Ala His	1590
505 510 515	
GGG GTA CCG CCG CCT GAT GTG ATC TGC GTG CGC TCT GGA GAA CTC GGG Gly Val Pro Pro Asp Val Ile Cys Val Arg Ser Ser Gly Glu Leu Gly	1638
520 525 530	
GCC GTC ATC GAG GGG CTG TTG CGT GTG GCC CGG GAG CAT GCG GGC ACT Ala Val Ile Glu Gly Leu Leu Arg Val Ala Arg Glu His Ala Gly Thr	1686
535 540 545	
TAC CGC TGC GAA GCC ACC AAC CCT CGG GGC TCT GCG GCC AAA AAT GTG Tyr Arg Cys Glu Ala Thr Asn Pro Arg Gly Ser Ala Lys Asn Val	1734
550 555 560 565	
GCC GTC ACG GTG GAA TAT GGC CCC AGG TTT GAG GAG CCG AGC TGC CCC Ala Val Thr Val Glu Tyr Gly Pro Arg Phe Glu Glu Pro Ser Cys Pro	1782
570 575 580	
AGC AAT TGG ACA TGG GTG GAA GGA TCT GGG CGC CTG TTT TCC TGT GAG Ser Asn Trp Thr Trp Val Glu Gly Ser Gly Arg Leu Phe Ser Cys Glu	1830
585 590 595	

GTC Val	GAT Asp	GGG Gly	AAG Lys	CCA Pro	CAG Gln	CCA Pro	AGC Ser	GTG Val	AAG Lys	TGC Cys	GTG Val	GGC Gly	TCC Ser	GGG Gly	GGC Gly	1878
600							605				610					
ACC Thr	ACT Thr	GAG Glu	GGG Gly	GTG Val	CTG Leu	CTG Leu	CCG Pro	CTG Leu	GCA Ala	CCC Pro	CCA Pro	GAC Pro	CCT Pro	AGT Ser	CCC Pro	1926
615						620				625						
AGA Arg	GCT Ala	CCC Pro	AGA Arg	ATC Ile	CCT Pro	AGA Arg	GTC Val	CTG Leu	GCA Ala	CCC Pro	GGT Gly	ATC Ile	TAC Tyr	GTG Val	TGC Cys	1974
630					635					640					645	
AAC Asn	GCC Ala	ACC Thr	AAC Asn	CGC Arg	CAC His	GGC Gly	TCC Ser	GTG Val	GCC Ala	AAA Lys	ACA Thr	GTC Val	GTG Val	AGC Ser	AGC Ser	2022
650									655					660		
GCG Ala	GAG Glu	TCG Ser	CCA Pro	CCG Pro	GAG Glu	ATG Met	GAT Asp	GAA Glu	TCT Ser	ACC Thr	TGC Cys	CCA Pro	AGT His	CAC Gln	CAG Gln	2070
665								670					675			
ACG Thr	TGG Trp	CTG Leu	GAA Glu	GGG Gly	GCT Ala	GAG Glu	GCT Ala	TCC Ser	GCG Ala	CTG Leu	GCC Ala	TGC Ala	GCC Ala	CGG Ala	CGG Arg	2118
680							685					690				
GGT Gly	CGC Arg	CCT Pro	TCC Ser	CCA Pro	GGA Gly	GTG Val	CGC Arg	TGC Cys	TCT Ser	CGG Arg	GAA Glu	GGC Gly	ATC Ile	CCA Pro	TGG Trp	2166
695						700					705					
CCT Pro	GAG Glu	CAG Gln	CAG Gln	CGC Arg	GTG Val	TCC Ser	CGA Arg	GAG Glu	GAC Asp	GCG Ala	GGC Gly	ACT Thr	TAC Tyr	CAC His	TGT Cys	2214
710					715					720					725	
GTG Val	GCC Ala	ACC Thr	AAT Asn	GCG His	CAT His	GGC Gly	ACG Thr	GAC Asp	TCC Ser	CGG Arg	ACC Thr	GTC Val	ACT Thr	GTG Val	GGC Gly	2262
730								735						740		
GTG Val	GAA Glu	TAC Tyr	CGG Arg	CCA Pro	GTG Val	GTG Val	GCC Ala	GAA Glu	CTT Leu	GCT Ala	GCC Ala	TCG Ser	CCC Pro	CCT Pro	GGA Gly	2310
745							750						755			
GGC Gly	GTG Val	CGC Arg	CCA Pro	GGA Gly	GGA Gly	AAC Asn	TTC Phe	ACG Thr	TTG Leu	ACC Thr	TGC Cys	CGC Arg	GCG Ala	GAG Glu	GCC Ala	2358
760							765				770					
TGG Trp	CCT Pro	CCA Pro	GCC Ala	CAG Gln	ATC Ile	AGC Ser	TGG Trp	CGC Arg	GCG Ala	CCC Pro	CCG Pro	AGG Arg	GCC Ala	CTC Leu	AAC Asn	2406
775						780					785					
ATC Ile	GGC Gly	CTG Leu	TCG Ser	AGC Ser	AAC Ser	AAC Asn	AGC Ser	ACA Thr	CTG Leu	AGC Ser	GTG Val	GCA Ala	GGC Gly	GCC Ala	ATG Met	2454
790					795					800					805	
GGA Gly	AGC Ser	CAC His	GGC Gly	GGC Gly	GAG Glu	TAC Tyr	GAG Glu	TGC Cys	GCA Ala	CGC Arg	ACC Thr	AAC Asn	GCG Ala	CAC His	GGG Gly	2502
810									815					820		
CGC Arg	CAC His	GCG Ala	CGG Arg	CGC Arg	ATC Ile	ACG Thr	GTG Val	CGC Arg	GTG Val	GCC Ala	GGT Gly	CCG Pro	TGG Trp	CTA Leu	TGG Trp	2550
825							830						835			
GTC Val	GCC Ala	GTG Val	GGC Gly	GGC Gly	GCG Ala	GCG Ala	GGG Gly	GCG Gly	GCG Ala	CTG Ala	CTG Leu	GCC Ala	GCG Ala	GGG Gly	GGG Gly	2598
840							845				850					

GCC GGC CTG GCC TTC TAC GTG CAG TCC ACC GCC TGC AAG AAG GGC GAG 2646
Ala Gly Leu Ala Phe Tyr Val Gln Ser Thr Ala Cys Lys Lys Gly Glu
855 860 865

TAC AAC GTG CAG GAG GCC GAG AGC TCA GGC GAG GGC GTG TGT CTG AAC 2694
Tyr Asn Val Gln Glu Ala Glu Ser Ser Gly Glu Ala Val Cys Leu Asn
870 875 880 885

GGA GCG GGC GGC GGC GCT GGC GGG GCG GCA GGC GCG GAG GGC GGA CCC 2742
Gly Ala Gly Gly Gly Ala Gly Gly Ala Glu Gly Gly Gly Pro
890 895 900

GAG GCG GCG GGG GGC GCG GCC GAG TCG CCG GCG GAG GGC GAG GTC TTC 2790
Glu Ala Ala Gly Gly Ala Ala Glu Ser Pro Ala Glu Gly Glu Val Phe
905 910 915

GCC ATA CAG CTG ACA TCG GCG TGAGCCCGCT CCCTCTCCG CGGGCCGGGA 2841
Ala Ile Gln Leu Thr Ser Ala
920 925

CGCCCCCAG ACTCACACGG GGGCTTATT ATTGCTTAT TTATTACTT ATTCATTTAT 2901

TTATGTATTC AACTCCAAGG GAATTC 2927

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Pro Gly Pro Ser Pro Gly Leu Arg Arg Ala Leu Leu Gly Leu Trp
1 5 10 15
Ala Ala Leu Gly Leu Gly Leu Phe Gly Leu Ser Ala Val Ser Gln Glu
20 25 30
Pro Phe Trp Ala Asp Leu Gln Pro Arg Val Ala Phe Val Glu Arg Gly
35 40 45
Gly Ser Leu Trp Leu Asn Cys Ser Thr Asn Cys Pro Arg Pro Glu Arg
50 55 60
Gly Gly Leu Glu Thr Ser Leu Arg Arg Asn Gly Thr Gln Arg Gly Leu
65 70 75 80
Arg Trp Leu Ala Arg Gln Leu Val Asp Ile Arg Glu Pro Glu Thr Gln
85 90 95
Pro Val Cys Phe Phe Arg Cys Ala Arg Arg Thr Leu Gln Ala Arg Gly
100 105 110
Leu Ile Arg Thr Phe Gln Arg Pro Asp Arg Val Glu Leu Met Pro Leu
115 120 125
Pro Pro Trp Gln Pro Val Gly Glu Asn Phe Thr Leu Ser Cys Arg Val
130 135 140

Pro Gly Ala Gly Pro Arg Ala Ser Leu Thr Leu Thr Leu Leu Arg Gly
145 150 155 160

Ala Gln Glu Leu Ile Arg Arg Ser Phe Ala Gly Glu Pro Pro Arg Ala
165 170 175

Arg Gly Ala Val Leu Thr Ala Thr Val Leu Ala Arg Arg Glu Asp His
180 185 190

Gly Ala Asn Phe Ser Cys Arg Ala Glu Leu Asp Leu Arg Pro His Gly
195 200 205

Leu Gly Leu Phe Glu Asn Ser Ser Ala Pro Arg Glu Leu Arg Thr Phe
210 215 220

Ser Leu Ser Pro Asp Ala Pro Arg Leu Ala Pro Arg Leu Leu Glu
225 230 235 240

Val Gly Ser Glu Arg Pro Val Ser Cys Thr Leu Asp Gly Leu Phe Pro
245 250 255

Ala Ser Glu Ala Arg Val Tyr Leu Ala Leu Gly Asp Gln Asn Leu Ser
260 265 270

Pro Asp Val Thr Leu Glu Gly Asp Ala Phe Val Ala Thr Ala Thr Ala
275 280 285

Thr Ala Ser Ala Glu Gln Glu Gly Ala Arg Gln Leu Val Cys Asn Val
290 295 300

Thr Leu Gly Gly Glu Asn Arg Glu Thr Arg Glu Asn Val Thr Ile Tyr
305 310 315 320

Ser Phe Pro Ala Pro Leu Leu Thr Leu Ser Glu Pro Ser Val Ser Glu
325 330 335

Gly Gln Met Val Thr Val Thr Cys Ala Ala Gly Ala Gln Ala Leu Val
340 345 350

Thr Leu Glu Gly Val Pro Ala Ala Val Pro Gly Gln Pro Ala Gln Leu
355 360 365

Gln Leu Asn Ala Thr Glu Asn Asp Asp Arg Arg Ser Phe Phe Cys Asp
370 375 380

Ala Thr Leu Asp Val Asp Gly Glu Thr Leu Ile Lys Asn Arg Ser Ala
385 390 395 400

Glu Leu Arg Val Leu Tyr Ala Pro Arg Leu Asp Asp Ser Asp Cys Pro
405 410 415

Arg Ser Trp Thr Trp Pro Glu Gly Pro Glu Gln Thr Leu Arg Cys Glu
420 425 430

Ala Arg Gly Asn Pro Glu Pro Ser Val His Cys Ala Arg Ser Asp Gly
435 440 445

Gly Ala Val Leu Ala Leu Gly Leu Leu Gly Pro Val Thr Arg Ala Leu
450 455 460

Ser Gly Thr Tyr Arg Cys Lys Ala Ala Asn Asp Gln Gly Glu Ala Val
465 470 475 480

Lys Asp Val Thr Leu Thr Val Glu Tyr Ala Pro Ala Leu Asp Ser Val
 485 490 495
 Gly Cys Pro Glu Arg Ile Thr Trp Leu Glu Gly Thr Glu Ala Ser Leu
 500 505 510
 Ser Cys Val Ala His Gly Val Pro Pro Pro Asp Val Ile Cys Val Arg
 515 520 525
 Ser Gly Glu Leu Gly Ala Val Ile Glu Gly Leu Leu Arg Val Ala Arg
 530 535 540
 Glu His Ala Gly Thr Tyr Arg Cys Glu Ala Thr Asn Pro Arg Gly Ser
 545 550 555 560
 Ala Ala Lys Asn Val Ala Val Thr Val Glu Tyr Gly Pro Arg Phe Glu
 565 570 575
 Glu Pro Ser Cys Pro Ser Asn Trp Thr Trp Val Glu Gly Ser Gly Arg
 580 585 590
 Leu Phe Ser Cys Glu Val Asp Gly Lys Pro Gln Pro Ser Val Lys Cys
 595 600 605
 Val Gly Ser Gly Gly Thr Thr Glu Gly Val Leu Leu Pro Leu Ala Pro
 610 615 620
 Pro Asp Pro Ser Pro Arg Ala Pro Arg Ile Pro Arg Val Leu Ala Pro
 625 630 635 640
 Gly Ile Tyr Val Cys Asn Ala Thr Asn Arg His Gly Ser Val Ala Lys
 645 650 655
 Thr Val Val Val Ser Ala Glu Ser Pro Pro Glu Met Asp Glu Ser Thr
 660 665 670
 Cys Pro Ser His Gln Thr Trp Leu Glu Gly Ala Glu Ala Ser Ala Leu
 675 680 685
 Ala Cys Ala Ala Arg Gly Arg Pro Ser Pro Gly Val Arg Cys Ser Arg
 690 695 700
 Glu Gly Ile Pro Trp Pro Glu Gln Gln Arg Val Ser Arg Glu Asp Ala
 705 710 715 720
 Gly Thr Tyr His Cys Val Ala Thr Asn Ala His Gly Thr Asp Ser Arg
 725 730 735
 Thr Val Thr Val Gly Val Glu Tyr Arg Pro Val Val Ala Glu Leu Ala
 740 745 750
 Ala Ser Pro Pro Gly Gly Val Arg Pro Gly Gly Asn Phe Thr Leu Thr
 755 760 765
 Cys Arg Ala Glu Ala Trp Pro Pro Ala Gln Ile Ser Trp Arg Ala Pro
 770 775 780
 Pro Arg Ala Leu Asn Ile Gly Leu Ser Ser Asn Asn Ser Thr Leu Ser
 785 790 795 800
 Val Ala Gly Ala Met Gly Ser His Gly Gly Glu Tyr Glu Cys Ala Arg
 805 810 815

Thr Asn Ala His Gly Arg His Ala Arg Arg Ile Thr Val Arg Val Ala
820 825
Gly Pro Trp Leu Trp Val Ala Val Gly Gly Ala Ala Gly Gly Ala Ala
835 840
Leu Leu Ala Ala Gly Ala Gly Leu Ala Phe Tyr Val Gln Ser Thr Ala
850 855
Cys Lys Lys Gly Glu Tyr Asn Val Gln Glu Ala Glu Ser Ser Gly Glu
865 870 875
Ala Val Cys Leu Asn Gly Ala Gly Gly Gly Ala Gly Gly Ala Ala Gly
885 890 895
Ala Glu Gly Gly Pro Glu Ala Ala Gly Gly Ala Ala Glu Ser Pro Ala
900 905 910
Glu Gly Glu Val Phe Ala Ile Gln Leu Thr Ser Ala
915 920

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTACTTACAG GATCCGCGGT CTCGCAGGAG CCTTCTGGG CGGACCTACA GCCTGCGTGG 60
CGTTC 65

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATTTCCTCG AGGATGGTCA CGTTCTCCCG G 31

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATTTCCTGGAT CCTACAGCTT CCGGCACCA CTC

33

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATTTCCTCG AGTCCACGC CCACAGTGAC GG

32

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1687 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGATCCTTTC	AGCCCTGAAA	GTCGAGGTTG	CAGTGAGCCT	TGATCGTGCC	ACTGCACCTCC	60
AGCCTGGGGG	ACAGAGCAGC	ACCCCTGTCT	CAAAAAATAA	ATAAAAAATAA	AAATAAATAT	120
TGGCGGGGGA	ACCCCTCTGA	ATCAATAAAG	GCTTCCTTAA	CCAGCCTCTG	TCCTGTGACC	180
TAAGGGTCCG	CATTACTGCC	CTTCTTCGGA	GGAAGTGTTT	TGTTTTTGTG	GTTGTTGTTG	240
TTTTTTCGAT	CATTCTCTCC	AAGTTCCTTG	TCTCCCTGAG	GGCACCTGAG	GTTTCTCTCAC	300
TCAGGGCCCA	CCTGGGGTCC	CGAAGCCCCA	GACTCTGTGT	ATCCCCAGCG	GGTGTACACAG	360
AAACCTCTCC	TTCTGCTGGC	CTTATCGAGT	GGGATCAGCG	CGGCCGGGGA	GAGCCACGGG	420
CAGGGCGGGG	GTGGGGTTCA	TGGTATGGCT	TTCTCTGATT	GCGCCGCCGC	CACCACGCGG	480
CAGCTCTGAT	TGGATGTTAA	GTTTCTCTAT	CCAGCCCCAC	CTTCAGACCC	TGTGCTTTCC	540
TGGAGGCCAA	ACAACCTGTG	AGCGAGAACT	CATCTCCAAA	ATAACTTACC	ACGCTGGAGT	600
GAGACCACGA	ATGGTGGGGA	GGGGAGGGTC	CCACGGACAT	ATTGAGGGAC	GTGGATACGC	660
AGAAGAGGTA	TCCATGTGGT	GGCAGCCGGG	AAGGGGTGAT	CAGATGTTCC	ACAGGGAATA	720
TCACAAACTC	GAATTCCTGAC	GATGTTCTGG	TAGTCACCCA	GCCAGATGAG	CGCATGGAGT	780
TGGCGGTGGG	GGGTGTCAAA	GCTTGGGGCC	CGGAAGCGGA	GTCAAAAGCA	TCACCTCTCG	840
TCCCTTGTTT	TCGCGTGGAT	GTCAGGGCCT	CCACCCACCG	AGCAGAAGGC	GGACTCAGGG	900
GCGCTCCAGG	GTGGCTCGAG	CTCACACACG	CTGAGTAGAC	ACGTGCCCGC	TGCACCTTGG	960
GTAAATACAG	ACCCGGAGCC	GAGCGGATTC	TAATTTAGAC	GCCCCGCAAC	GCTGCGCGCA	1020
CGCACACGTG	TCCTCGGCTC	GCTGGCACTT	TCGTCCCGCC	CCCTCCGTCG	CGTGCCGGAG	1080

CTGACCCGGA GGGGTGCTTA GAGGTATGGC TCCGCGGGGT CAAAGGAGA AGGATCAGTG	1140
AGAGAGGATC CCCACACCT CCCCTAGAAC TGTCCTTTCC CCATCCAGTG CCTCCCAAAT	1200
CTCTCTTAGT CCCCAAATGT ATCCCCGCC TAAGGGGCGC TGGTGGGAGG AGCTAAATGT	1260
GGGGGCGGAG CTCGGAGTCC AGCTTATTAT CATGGCATCT CAGCCAGGGG TGGGGTAGGG	1320
GTTTGGGAAG GGCAACCCAG CATCCCCGGA TCCAGAGTC GCGGCCGGGG ATGACGCGAG	1380
AGAGCGTGGT CGCCCCCAGA AGGCCCTGGG CCATCATGCC GGCCTCCACG TAGACCCAG	1440
GGGTGCTCA CTCCTGCCAG CTCGCCTTCA CCAAGGCCAG GAGCTTAGCG CACGCTGCC	1500
TCCCGCCCC CCGCCGCCTC TGCCGCCGCC CCTCCTTGG AACCAAGTT ACCAACGTTA	1560
AACCAATCCC CAAGCGCAAC TCTGTCTCCC CCACACCCCA CCGCCGCGC CGCGCGGAGC	1620
CGTCTCTAG CCCAGCTCCT CGGCTCGGCC TCTCCTCGCC TCCTGTGCTT TCCCCCGCC	1680
GGCGATG	1687

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CAGAACTAAG CTTACAGGAG GCGAGGAGAG CGCGAG	36
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(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CAACAATGCT AGCCAAGCGC AACTCTGTCT C	31
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(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAACAATGCT AGCCTTGGA ACCAAGTTAC C	31
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(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAACAATGCT AGCAGGAGCT TAGCGCACGC TCG

33

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CAACAATGCT AGCCATGCCG GCCTCCACGT AG

32

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CAACAATGCT AGCGTCCAGC TTATTATCAT G

31

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CAACAATGCT AGCCTTAGTC CCCAAATGTA TC

32

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CAACAATGCT AGCGGAGAAG GATCAGTGAG

30

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CAACAATGCT AGCCTCCACC CACCGAGCAG AAG

33

CAACAATGCT AGCCTCCACC CACCGAGCAG AAG